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(54) Title: ANTI-BACTERIAL VACCINE COMPOSITIONS

(57) Abstract: Gram negative bacterial virulence genes are identified, thereby allowing the identification of novel anti-bacterial agents that target these virulence genes and their products, and the provision of novel gram negative bacterial mutants useful in vaccines.

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## ANTI-BACTERIAL VACCINE COMPOSITIONS

This application is a continuation-in-part of U.S. Patent Application Serial No: 09/545,199, filed April 6, 2000, which claims benefit of U.S. Provisional Patent Application Serial Nos. 60/153,453, filed September 10, 1999 and 60/128,689, filed April 9, 1999.

### FIELD OF THE INVENTION

The present invention relates generally to the identification of genes responsible for virulence of *Pasteurellaceae* bacteria, thereby allowing for production of novel attenuated mutant strains useful in vaccines and identification of new anti-bacterial agents that target the virulence genes and their products.

### BACKGROUND OF THE INVENTION

The family *Pasteurellaceae* encompasses several significant pathogens that infect a wide variety of animals. In addition to *P. multocida*, prominent members of the family include *Pasteurella (Mannheimia) haemolytica*, *Actinobacillus pleuropneumoniae* and *Haemophilus somnus*. *P. multocida* is a gram-negative, nonmotile coccobacillus which is found in the normal flora of many wild and domestic animals and is known to cause disease in numerous animal species worldwide [Biberstein, In M. Kilian, W. Frederickson, and E. L. Biberstein (ed.), *Haemophilus, Pasteurella, and Actinobacillus*. Academic Press, London, p. 61-73 (1981)]. The disease manifestations following infection include septicemias, bronchopneumonias, rhinitis, and wound infections [Reviewed in Shewen, *et al.*, In C. L. Gyles and C. O. Thoen (ed.), *Pathogenesis of Bacterial Infections in Animals*. Iowa State University Press, Ames, p. 216-225 (1993), incorporated herein by reference].

Infection by *P. multocida* generally results from invasion during periods of stress, but transmission may also occur by aerosol or contact exposure, or via flea and tick vectors. In fowl, *P. multocida* infection gives rise to acute to peracute septicemia, particularly prevalent in domestic turkeys and wild waterfowl under stress conditions associated with overcrowding, laying, molting, or severe

climatic change. In cattle, a similar hemorrhagic septicemia follows infection and manifests conditions including high fever and depression, generally followed by quick death. Transmission is most likely through aerosol contact, but infection can also arise during periods of significant climatic change. In rabbits, infection gives rise to recurring purulent rhinitis, generally followed by conjunctivitis, otitis media, sinusitis, subcutaneous abscesses, and chronic bronchopneumonia. In severe infections, rabbit mortality arises from acute fibrinous bronchopneumonia, septicemia, or endotoxemia. Disease states normally arise during periods of stress. In pigs, common *P. multocida* disease states include atrophic rhinitis and bacterial pneumonia. Similar pneumonia conditions are also detected in dogs, cats, goats, and sheep. *P. multocida* is commonly detected in oral flora of many animals and is therefore a common contaminant in bite and scratch wounds.

*P. multocida* strains are normally designated by capsular serogroup and somatic serotype. Five capsular serogroups (A, B, D, E, and F) and 16 somatic serotypes are distinguished by expression of characteristic heat-stable antigens. Most strains are host specific and rarely infect more than one or two animals. The existence of different serotypes presents a problem for vaccination because traditional killed whole cell bacteria normally provide only serotype-specific protection. However, it has been demonstrated that natural infection with one serotype can lead to immunological protection against multiple serotypes [Shewen, *et al.*, In C. L. Gyles and C. O. Thoen (Ed.), Pathogenesis of Bacterial Infections in Animals. Iowa State University Press, Ames, p. 216-225 (1993)] and cross protection can also be stimulated by using inactivated bacteria grown *in vivo* [Rimler, *et al.*, *Am J Vet Res.* 42:2117-2121 (1981)]. One live spontaneous mutant *P. multocida* strain has been utilized as a vaccine and has been shown to stimulate a strong immune response [Davis, *Poultry Digest.* 20:430-434 (1987), Schlink, *et al.*, *Avian Dis.* 31(1):13-21 (1987)]. This attenuated strain, however, has been shown to revert to a virulent state or cause mortality if the vaccine recipient is stressed [Davis, *Poultry Digest.* 20:430-434 (1987), Schlink, *et al.*, *Avian Dis.* 31(1):13-21 (1987)].

Another member of the *Pasteurella* family, *A. pleuropneumoniae* exhibits strict host specificity for swine and is the causative agent of highly contagious porcine pleuropneumonia. Infection normally arises in intensive breeding conditions, and is believed to occur by a direct mode of transmission. The disease is often fatal and, as a result, leads to severe economic loss in the swine producing industry. *A. pleuropneumoniae* infection may be chronic or acute, and infection is characterized by a hemorrhagic, necrotic bronchopneumonia with accompanying fibrinous pleuritis. To date, bacterial virulence has been attributed to structural proteins, including serotype-specific capsular polysaccharides, lipopolysaccharides, and surface proteins, as well as extracellular cytolytic toxins. Despite purification and, in some instances cloning, of these virulence factors, the exact role of these virulence factors in *A. pleuropneumoniae* infection is poorly understood.

Twelve serotypes of *A. pleuropneumoniae* have been identified based on antigenic differences in capsular polysaccharides and production of extracellular toxins. Serotypes 1, 5, and 7 are most relevant to *A. pleuropneumoniae* infection in the United States, while serotypes 1, 2, 5, 7, and 9 are predominant in Europe. There are at least three significant extracellular toxins of *A. pleuropneumoniae* that are members of the haemolysin family and are referred to as RTX toxins. RTX toxins are produced by many Gram negative bacteria, including *E. coli*, *Proteus vulgaris*, and *Pasteurella haemolytica*, and the proteins generally share structural and functional characteristics. Toxins from the various serotypes differ, however, in host specificity, target cells, and biological activities.

The major *A. pleuropneumoniae* RTX toxins include ApxI, ApxII, and ApxIII. ApxI and ApxII have haemolytic activity, with ApxI being more potent. ApxIII shows no haemolytic activity, but is cytotoxic for alveolar macrophages and neutrophils. Most *A. pleuropneumoniae* serotypes produce two of these three toxins. For example, serotypes 1, 5, 9, and 11 express ApxI and ApxII, and serotypes 2, 3, 4, 6, and 8 express ApxII and ApxIII. Serotype 10, however, produces only ApxI, and serotypes 7 and 12 express only ApxII. Those *A. pleuropneumoniae* serotypes that produce both ApxI and ApxII are the most virulent strains of the bacteria.

The Apx toxins were demonstrated to be virulence factors in murine models and swine infection using randomly mutated wild type bacteria [Tascon, *et al.*, *Mol. Microbiol.* 14:207-216 (1994)]. Other *A. pleuropneumoniae* mutants have also been generated with targeted mutagenesis to inactivate the gene encoding the AopA outer membrane virulence protein [Mulks and Buysee, *Gene* 165:61-66 (1995)].

At least eleven serotypes (1, 2, 5-9, 12-14 and 16) have been demonstrated within *Mannheimia* [*Pasteurella*] *haemolytica* [Angen, *et al.*, *Vet Microbiol* 65(4):283-90 (1999)], a *Pasteurellaceae* species which is responsible for serious outbreaks of acute pneumonia in neonatal, weaned, growing and adult lambs, calves, and goats [Ackermann, *et al.*, *Microbes Infect* 2(9):1079-88 (2000)]. Transportation, viral infections, overcrowding, and other stressful conditions predispose animals to *M. haemolytica* infection [Ackermann, *et al.*, *supra.*] The leukotoxin (Lkt) of *M. haemolytica* is believed to play a significant role in pathogenesis, causing cell lysis and apoptosis that lead to the lung pathology characteristic of bovine shipping fever [Highlander, *et al.*, *Infect Immun* 68(7):3916-22 (2000)] as well as lung injury in bovine pneumonic pasteurellosis [Jeyaseelan, *et al.*, *Microb Pathog* 30(2):59-69 (2001)]. Lkt is a pore-forming exotoxin that has the unique property of inducing cytolysis only in ruminant leukocytes and platelets [Jeyaseelan, *et al.*, (2001), *supra.*]. Cytolysis of many cell types is mediated by arachidonic acid (AA) and its generation by phospholipases is regulated by G-protein-coupled receptors [Jeyaseelan, *et al.*, (2001) *supra.*] Recent studies indicate that *M. haemolytica* Lkt binds to bovine CD18, the common subunit of all beta2 integrins [Jeyaseelan, *et al.*, *Infect Immun* 68(1):72-9 (2000)]. It has also been shown that LFA-1 is a Lkt receptor, Lkt binding to LFA-1 is not target cell specific, Lkt binding to bovine LFA-1 correlates with calcium elevation and cytolysis, and bovine LFA-1 expression correlates with the magnitude of Lkt-induced target cell cytolysis [Jeyaseelan, *et al.*, *Infect Immun* 68(1):72-9 (2000)].

In attempts to produce vaccine compositions, traditional killed whole cell bacteria have provided only serotype-specific protection [MacInnes and Smart, *supra*], however, it has been demonstrated that natural infection with a highly virulent

serotype can stimulate strong protective immunity against multiple serotypes [Nielsen, *Nord Vet Med.* 31:407-13 (1979), Nielsen, *Nord Vet Med.* 36:221-234 (1984), Nielsen, *Can J Vet Res.* 29:580-582 (1988), Nielsen, *ACTA Vet Scand.* 15:80-89 (1994)]. One defined live-attenuated vaccine strain producing an inactive form of the ApxII toxin has shown promise for cross protection in swine [Prideaux, *et al.*, *Infection & Immunity* 67:1962-1966 (1999)], while other undefined live-attenuated mutants have also shown promise [Inzana, *et al.*, *Infect Immun.* 61:1682-6, (1993), Paltineanu, *et al.*, *In International Pig Veterinary Society*, 1992, p. 214, Utrera, *et al.*, *In International Pig Veterinary Society*, 1992, p. 213].

Because of the problems associated with vaccine formulations comprising bacterial strains with undefined, spontaneous mutations, there exists a need in the art for rational construction of live attenuated bacterial strains for use in vaccines that will safely stimulate protective immunity against homologous and heterologous *Pasteurellaceae* serotypes. There further exists a need to identify attenuated bacterial strains and genes required for bacterial virulence, thereby facilitating development of methods to identify anti-bacterial agents.

## SUMMARY OF THE INVENTION

In general, the present invention provides materials and methods for production and use of vaccine compositions comprising attenuated gram negative bacteria. In one aspect, vaccine compositions of the invention comprise attenuated species in the *Pasteurellaceae* family of bacteria, which is known in the art and described, in part, in Dewhirst, *et al.*, *J. Bacteriol.* 174:2002-2013 (1992), incorporated herein by reference in its entirety. Species in the family include, but are not limited to, *A. actinomycetemcomitans*, *A. capsulatus*, *A. equuli*, *A. lignieresii*, *A. pleuropneumoniae* (*H. pleuropneumoniae*), *A. seminis*, *A. suis* (*H. suis*), *A. ureae* (*p. ureae*), *A. capsulatus*, Bisgaard taxon 11, *H. aegyptius*, *H. aphrophilus*, *H. aphrophilus* (*H. parainfluenzae*), *H. ducreyi*, *H. haemoglobinophilus*, *H. haemolyticus*, *H. influenzae*, *H. paracuniculus*, *H. paragallinarum*, *H. parahaemolyticus*, *H. parainfluenzae*, (*H. paraphrophilus*), *H.*

*paraphrohaemolyticus*, *H. paraphrophilus*, *H. parasuis*, *H. parasuis* type 5, *H. segnis*,  
*H. somnus*, *Haemophilus* minor group, *Haemophilus* taxon C, *P. aerogenes*, *P. anatis*,  
*P. avium* (*H. avium*), *P. canis*, *P. dagmatis*, *P. gallinarum*, *P. (Mannheimia)*  
*haemolytica*, *P. trehalosi* (*P. haemolytica* biotype T), *P. langaa*, *P. multocida*, *P.*  
5 *pneumotropica*, *P. stomatis*, *P. volantium* (*H. parainfluenzae*), *P. volantium*,  
*Pasteurella* species A, *Pasteurella* species B, and *Haemophilus*  
*paraphrohaemolyticus*. Preferably, vaccine compositions comprise attenuated  
*Pasteurella (Mannheimia) haemolytica*, *Actinobacillus pleuropneumoniae*,  
*Haemophilus somnus*, or *Pasteurella multocida* bacteria. In a most preferred  
10 embodiment, vaccine compositions of the invention comprise attenuated *Pasteurella*  
*multocida* and *A. plueropneumoniae* bacterial strains.

One aspect of the invention provides gram negative bacterial  
 organisms containing a functional mutation in a gene sequence represented by any one  
 of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51,  
 15 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110,  
 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142,  
 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and  
 174, or species homologs thereof, wherein the mutation inhibits or abolishes  
 expression and/or biological activity of an encoded gene product (*i.e.*, the polypeptide  
 20 encoded by a gene); said functional mutation resulting in attenuated virulence of the  
 bacterial strain. Functional mutations that modulate (*i.e.*, increase or decrease)  
 expression and/or biological activity of a gene product include insertions or deletions  
 in the protein coding region of the gene itself or in sequences responsible for, or  
 involved in, control of gene expression. Deletion mutants include those wherein all or  
 25 part of a specific gene sequence is deleted. Also contemplated are compositions, and  
 preferably vaccine compositions, comprising mutated and attenuated gram negative  
 bacterial organisms, optionally comprising a suitable adjuvant and/or a  
 pharmaceutically acceptable diluent or carrier. In order for a modified strain to be  
 effective in a vaccine formulation, the attenuation must be significant enough to

prevent the pathogen from evoking severe clinical symptoms, but also insignificant enough to allow limited replication and growth of the bacteria in the host.

The invention also provides polynucleotides encoding gene products that are required for virulence in gram negative bacteria. Polynucleotides of the invention include DNA, such as complementary DNA, genomic DNA including complementary or anti-sense DNA, and wholly or partially synthesized DNA; RNA, including sense and antisense strands; and peptide nucleic acids as described, for example in Corey, *TIBTECH* 15:224-229 (1997). Virulence gene polynucleotides of the invention include those set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or species homologs thereof, polynucleotides encoding a virulence gene product encoded by a polynucleotide of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or a species homolog thereof, and polynucleotide that hybridize, under moderately to highly stringent conditions, to the noncoding strand (or complement) of any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or species homologs thereof. The invention therefore comprehends gene sequences from *Pasteurellaceae* set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, as well as related gene sequences from other

gram negative bacterial organisms, including naturally occurring (*i.e.*, species homologs) and artificially induced variants thereof. The invention also comprehends polynucleotides which encode polypeptides deduced from any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172, and 174, and species homologs thereof. Knowledge of the sequence of a polynucleotide of the invention makes readily available every possible fragment of that polynucleotide. The invention therefore provides fragments of a polynucleotide of the invention.

The invention further embraces expression constructs comprising polynucleotides of the invention. Host cells transformed, transfected or electroporated with a polynucleotide of the invention are also contemplated. The invention provides methods to produce a polypeptide encoded by a polynucleotide of the invention comprising the steps of growing a host cell of the invention under conditions that permit, and preferably promote, expression of a gene product encoded by the polynucleotide, and isolating the gene product from the host cell or the medium of its growth.

Identification of polynucleotides of the invention makes available the encoded polypeptides. Polypeptides of the invention include full length and fragment, or truncated, proteins; variants thereof; fusion, or chimeric proteins; and analogs, including those wherein conservative amino acid substitutions have been introduced into wild-type polypeptides. Antibodies that specifically recognize polypeptides of the invention are also provided, and include monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, humanized antibodies, human antibodies, and complementary determining region (CDR)-grafted antibodies, as well as compounds that include CDR sequences which specifically recognize a polypeptide of the invention. The invention also provides anti-idiotypic antibodies immunospecific for antibodies of the invention.

According to another aspect of the invention, methods are provided for identifying novel anti-bacterial agents that modulate the function of gram negative bacteria virulence genes or gene products. Methods of the invention include screening potential agents for the ability to interfere with expression of virulence gene products encoded by the DNA sequences set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or species homologs thereof, or screening potential agents for the ability to interfere with biological function of a bacterial gene product encoded in whole or in part by a DNA sequence set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, species homologs thereof, or the complementary strand thereof, followed by identifying agents that provide positive results in such screening assays. In particular, agents that interfere with the expression of virulence gene products include anti-sense polynucleotides and ribozymes that are complementary to the virulence gene sequences. The invention further embraces methods to modulate transcription of gene products of the invention through use of oligonucleotide-directed triplet helix formation.

Agents that interfere with the function of virulence gene products include variants of virulence gene products, binding partners of the virulence gene products and variants of such binding partners, and enzyme inhibitors (where the product is an enzyme).

Novel anti-bacterial agents identified by the methods described herein are provided, as well as methods for treating a subject suffering from infection with gram negative bacteria involving administration of such novel anti-bacterial agents in an amount effective to reduce bacterial presence.

Numerous additional aspects and advantages of the invention will become apparent to those skilled in the art upon consideration of the following detailed description of the invention which describes presently prepared embodiments thereof.

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## DETAILED DESCRIPTION OF THE INVENTION

"Virulence genes," as used herein, are genes whose function or products are required for successful establishment and/or maintenance of bacterial infection in a host animal. Thus, virulence genes and/or the proteins encoded thereby are involved in pathogenesis in the host organism, but may not be necessary for growth.

"Signature-tagged mutagenesis (STM)," as used herein, is a method generally described in International Patent Publication No. WO 96/17951, incorporated herein by reference, and includes, for example, a method for identifying bacterial genes required for virulence in a murine model of bacteremia. In this method, bacterial strains that each have a random mutation in the genome are produced using transposon integration; each insertional mutation carries a different DNA signature tag which allows mutants to be differentiated from each other. The tags comprise 40 bp variable central regions flanked by invariant "arms" of 20 bp which allow the central portions to be co-amplified by polymerase chain reaction (PCR). Tagged mutant strains are assembled in microtiter dishes, then combined to form the "inoculum pool" for infection studies. At an appropriate time after inoculation, bacteria are isolated from the animal and pooled to form the "recovered pool." The tags in the recovered pool and the tags in the inoculum pool are separately amplified, labeled, and then used to probe filters arrayed with all of the different tags representing the mutants in the inoculum. Mutant strains with attenuated virulence are those which cannot be recovered from the infected animal, *i.e.*, strains with tags that give hybridization signals when probed with tags from the inoculum pool but not when probed with tags from the recovered pool. In a variation of this method, non-radioactive detection methods such as chemiluminescence can be used

Signature-tagged mutagenesis allows a large number of insertional mutant strains to be screened simultaneously in a single animal for loss of virulence. Screening nineteen pools of mutant *P. multocida* strains resulted in the identification of more than 60 strains with reduced virulence, many of which were confirmed to be attenuated in virulence by subsequent determination of an approximate LD<sub>50</sub> for the individual mutants. Screening of *A. pleuropneumoniae* mutants resulted in identification of more than 100 strains having mutations in 35 different genes. Of these, mutations in 22 genes results in significantly attenuated *A. pleuropneumoniae* strains. The nucleotide sequence of the open reading frame disrupted by the transposon insertion was determined by sequencing both strands and an encoded amino acid sequence was deduced. Novelty of both the polynucleotide and amino acid sequences was determined by comparison of the sequences with DNA and protein database sequences. Knowledge of the virulence genes in these species permitted identification of species homologs in *P. (Mannheimia) haemolytica*.

The identification of bacterial, and more particularly *P. multocida* *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* virulence genes provides for microorganisms exhibiting reduced virulence (i.e., attenuated strains), which are useful in vaccines. Such microorganisms include *Pasteurellaceae* mutants containing at least one functional mutation inactivating a gene represented by any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174. The worker of ordinary skill in the art will realize that a "functional mutation" may occur in protein coding regions of a gene of the invention, as well as in regulatory regions that modulate transcription of the virulence gene RNA.

The worker of ordinary skill will also appreciate that attenuated *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* strains of the invention include those bearing more than one functional mutation. More than one mutation may result in additive or synergistic degrees of attenuation. Multiple

mutations can be prepared by design or may fortuitously arise from a deletion event originally intended to introduce a single mutation. An example of an attenuated strain with multiple deletions is a *Salmonella typhimurium* strain wherein the *cya* and *crp* genes are functionally deleted. This mutant *S. typhimurium* strain has shown promise as a live vaccine.

Identification of virulence genes in *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* can provide information regarding similar genes in other pathogenic species. As an example, identification of the *aroA* gene led to identification of conserved genes in a diverse number of pathogens, including *Aeromonas hydrophila*, *Aeromonas salmonicida*, *Salmonella typhimurium*, *Salmonella enteritidis*, *Salmonella dublin*, *Salmonella gallinarum*, *Bordetella pertussis*, *Yersinia enterocolitica*, *Neisseria gonorrhoeae*, and *Bacillus anthracis*. In many of these species, attenuated bacterial strains bearing mutations in the *aroA* gene have proven to be effective in vaccine formulations. Using the virulence genes sequences identified in *P. multocida*, similar or homologous genes can be identified in other organisms, particularly within the *Pasteurella* family, as well as *A. pleuropneumoniae*, *P. (Mannheimia) haemolytica*, and *Haemophilus somnus*. Likewise, identification of *A. pleuropneumoniae* virulence genes can permit identification of related genes in other organisms. Southern hybridization using the *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* genes as probes can identify these related genes in chromosomal libraries derived from other organisms. Alternatively, PCR can be equally effective in gene identification across species boundaries. As still another alternative, complementation of, for example, a *P. multocida* mutant with a chromosomal library from other species can also be used to identify genes having the same or related virulence activity. Identification of related virulence genes can therefore lead to production of an attenuated strain of the other organism which can be useful as still another vaccine formulation. Examples of *P. multocida* genes that have been demonstrated to exist in other species (e.g. *P. (Mannheimia) haemolytica*, *A. pleuropneumoniae* and *H. somnus*) include genes *exxB*, *atpG*, *pnp*, *guaB* and *yjgF*.

Attenuated *P. multocida* strains identified using STM are insertional mutants wherein a virulence gene has been rendered non-functional through insertion of transposon sequences in either the open reading frame or regulatory DNA sequences. These insertional mutants still contain all of the genetic information required for bacterial virulence and can possibly revert to a pathogenic state by deletion of the inserted transposon. Therefore, in preparing a vaccine formulation, it is desirable to take the information gleaned from the attenuated strain and create a deletion mutant strain wherein some, most, or all of the virulence gene sequence is removed, thereby precluding the possibility that the bacteria will revert to a virulent state.

The vaccine properties of an attenuated insertional mutant identified using STM are expected to be the same or similar to those of a bacteria bearing a deletion in the same gene. However, it is possible that an insertion mutation may exert "polar" effects on adjoining gene sequences, and as a result, the insertion mutant may possess characteristic distinct from a mutant strain with a deletion in the same gene sequence. Deletion mutants can be constructed using any of a number of techniques well known and routinely practiced in the art.

In one example, a strategy using counterselectable markers can be employed which has commonly been utilized to delete genes in many bacteria. For a review, see, for example, Reytrat, *et al.*, *Infection and Immunity* 66:4011-4017 (1998), incorporated herein by reference. In this technique, a double selection strategy is often employed wherein a plasmid is constructed encoding both a selectable and counterselectable marker, with flanking DNA sequences derived from both sides of the desired deletion. The selectable marker is used to select for bacteria in which the plasmid has integrated into the genome in the appropriate location and manner. The counterselectable marker is used to select for the very small percentage of bacteria that have spontaneously eliminated the integrated plasmid. A fraction of these bacteria will then contain only the desired deletion with no other foreign DNA present. The key to the use of this technique is the availability of a suitable counterselectable marker.

In another technique, the *cre-lox* system is used for site specific recombination of DNA. The system consists of 34 base pair *lox* sequences that are recognized by the bacterial *cre* recombinase gene. If the *lox* sites are present in the DNA in an appropriate orientation, DNA flanked by the *lox* sites will be excised by the *cre* recombinase, resulting in the deletion of all sequences except for one remaining copy of the *lox* sequence. Using standard recombination techniques, it is possible to delete the targeted gene of interest in the *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica* genome and to replace it with a selectable marker (e.g., a gene coding for kanamycin resistance) that is flanked by the *lox* sites. Transient expression (by electroporation of a suicide plasmid containing the *cre* gene under control of a promoter that functions in *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica*) of the *cre* recombinase should result in efficient elimination of the *lox* flanked marker. This process would result in a mutant containing the desired deletion mutation and one copy of the *lox* sequences.

In another approach, it is possible to directly replace a desired deleted sequence in the *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica* genome with a marker gene, such as green fluorescent protein (GFP),  $\beta$ -galactosidase, or luciferase. In this technique, DNA segments flanking a desired deletion are prepared by PCR and cloned into a suicide (non-replicating) vector for *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica*. An expression cassette, containing a promoter active in *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica* and the appropriate marker gene, is cloned between the flanking sequences. The plasmid is introduced into wild-type *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica*. Bacteria that incorporate and express the marker gene (probably at a very low frequency) are isolated and examined for the appropriate recombination event (i.e., replacement of the wild type gene with the marker gene).

The reduced virulence of these organisms and their immunogenicity may be confirmed by administration to a subject animal. While it is possible for an avirulent microorganism of the invention to be administered alone, one or more of

such mutant microorganisms are preferably administered in a vaccine composition containing suitable adjuvant(s) and pharmaceutically acceptable diluent(s) or carrier(s). The carrier(s) must be "acceptable" in the sense of being compatible with the avirulent microorganism of the invention and not deleterious to the subject to be immunized. Typically, the carriers will be water or saline which will be sterile and pyrogen free. The subject to be immunized is a subject needing protection from a disease caused by a virulent form of *P. multocida*, *A. pleuropneumoniae*, *P. (Mannheimia) haemolytica* or other pathogenic microorganisms.

It will be appreciated that the vaccine of the invention may be useful in the fields of human medicine and veterinary medicine. Thus, the subject to be immunized may be a human or other animal, for example, farm animals including cows, sheep, pigs, horses, goats and poultry (e.g., chickens, turkeys, ducks and geese) companion animals such as dogs and cats; exotic and/or zoo animals; and laboratory animals including mice, rats, rabbits, guinea pigs, and hamsters.

The invention also provides polypeptides and corresponding polynucleotides required for *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica* virulence. The invention includes both naturally occurring and non-naturally occurring polynucleotides and polypeptide products thereof. Naturally occurring virulence products include distinct gene and polypeptide species as well as corresponding species homologs expressed in organisms other than *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica* strains. Non-naturally occurring virulence products include variants of the naturally occurring products such as analogs and virulence products which include covalent modifications. In a preferred embodiment, the invention provides virulence polynucleotides comprising the sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs thereof, and polypeptides having amino acids sequences encoded by the polynucleotides.

The present invention provides novel purified and isolated *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* polynucleotides (e.g., DNA sequences and RNA transcripts, both sense and complementary antisense strands) encoding the bacterial virulence gene products. DNA sequences of the invention include genomic and cDNA sequences as well as wholly or partially chemically synthesized DNA sequences. Genomic DNA of the invention comprises the protein coding region for a polypeptide of the invention and includes variants that may be found in other bacterial strains of the same species. "Synthesized," as used herein and is understood in the art, refers to purely chemical, as opposed to enzymatic, methods for producing polynucleotides. "Wholly" synthesized DNA sequences are therefore produced entirely by chemical means, and "partially" synthesized DNAs embrace those wherein only portions of the resulting DNA were produced by chemical means. Preferred DNA sequences encoding *P. multocida* virulence gene products are set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, and species homologs thereof. Preferred *A. pleuropneumoniae* DNA sequences encoding virulence gene products are set out in SEQ ID NOs: 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof. Preferred *P. (Mannheimia) haemolytica* virulence gene products are set out in SEQ ID NOs: 166, 168, 170, 172 and 174, and species homologs thereof. The worker of skill in the art will readily appreciate that the preferred DNA of the invention comprises a double stranded molecule, for example, molecules having the sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs thereof, along with the complementary molecule (the "non-coding strand" or "complement") having a sequence deducible from the sequence of SEQ ID NO: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53,

55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, according to Watson-Crick base pairing rules for DNA. Also preferred are

5 polynucleotides encoding the gene products encoded by any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs thereof. The invention further embraces  
10 species, preferably bacterial, homologs of the *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* DNA.

The polynucleotide sequence information provided by the invention makes possible the identification and isolation of polynucleotides encoding related  
15 bacterial virulence molecules by well known techniques including Southern and/or Northern hybridization, and polymerase chain reaction (PCR). Examples of related polynucleotides include polynucleotides encoding polypeptides homologous to a virulence gene product encoded by any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, and species  
20 homologs thereof, and structurally related polypeptides sharing one or more biological and/or physical properties of a virulence gene product of the invention.

25 The invention also embraces DNA sequences encoding bacterial gene products which hybridize under moderately to highly stringent conditions to the non-coding strand, or complement, of any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146,  
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148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172 and 174, and species homologs thereof. DNA sequences encoding virulence polypeptides which would hybridize thereto but for the degeneracy of the genetic code are contemplated by the invention. Exemplary high stringency conditions include a final wash in buffer  
5 comprising 0.2X SSC/0.1% SDS, at 65°C to 75°C, while exemplary moderate stringency conditions include a final wash in buffer comprising 2X SSC/0.1% SDS, at 35°C to 45°C. It is understood in the art that conditions of equivalent stringency can be achieved through variation of temperature and buffer, or salt concentration as described in Ausubel, *et al.* (Eds.), Protocols in Molecular Biology, John Wiley &  
10 Sons (1994), pp. 6.0.3 to 6.4.10. Modifications in hybridization conditions can be empirically determined or precisely calculated based on the length and the percentage of guanine/cytosine (GC) base pairing of the probe. The hybridization conditions can be calculated as described in Sambrook, *et al.*, (Eds.), Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press: Cold Spring Harbor, New  
15 York (1989), pp. 9.47 to 9.51.

Autonomously replicating recombinant expression constructions such as plasmid and viral DNA vectors incorporating virulence gene sequences are also provided. Expression constructs wherein virulence polypeptide-encoding polynucleotides are operatively linked to an endogenous or exogenous expression  
20 control DNA sequence and a transcription terminator are also provided. The virulence genes may be cloned by PCR, using *P. multocida* genomic DNA as the template. For ease of inserting the gene into expression vectors, PCR primers are chosen so that the PCR-amplified gene has a restriction enzyme site at the 5' end preceding the initiation codon ATG, and a restriction enzyme site at the 3' end after  
25 the termination codon TAG, TGA or TAA. If desirable, the codons in the gene are changed, without changing the amino acids, according to *E. coli* codon preference described by Grosjean and Fiers, *Gene*, 18:199-209 (1982), and Konigsberg and Godson, *Proc. Natl. Acad. Sci. (USA)*, 80:687-691 (1983). Optimization of codon usage may lead to an increase in the expression of the gene product when produced in  
30 *E. coli*. If the gene product is to be produced extracellularly, either in the periplasm of

*E. coli* or other bacteria, or into the cell culture medium, the gene is cloned without its initiation codon and placed into an expression vector behind a signal sequence.

According to another aspect of the invention, host cells are provided, including procaryotic and eukaryotic cells, either stably or transiently transformed, transfected, or electroporated with polynucleotide sequences of the invention in a manner which permits expression of virulence polypeptides of the invention. Expression systems of the invention include bacterial, yeast, fungal, viral, invertebrate, and mammalian cells systems. Host cells of the invention are a valuable source of immunogen for development of antibodies specifically immunoreactive with the virulence gene product. Host cells of the invention are conspicuously useful in methods for large scale production of virulence polypeptides wherein the cells are grown in a suitable culture medium and the desired polypeptide products are isolated from the cells or from the medium in which the cells are grown by, for example, immunoaffinity purification or any of the multitude of purification techniques well known and routinely practiced in the art. Any suitable host cell may be used for expression of the gene product, such as *E. coli*, other bacteria, including *P. multocida*, *Bacillus* and *S. aureus*, yeast, including *Pichia pastoris* and *Saccharomyces cerevisiae*, insect cells, or mammalian cells, including CHO cells, utilizing suitable vectors known in the art. Proteins may be produced directly or fused to a peptide or polypeptide, and either intracellularly or extracellularly by secretion into the periplasmic space of a bacterial cell or into the cell culture medium. Secretion of a protein requires a signal peptide (also known as pre-sequence); a number of signal sequences from prokaryotes and eukaryotes are known to function for the secretion of recombinant proteins. During the protein secretion process, the signal peptide is removed by signal peptidase to yield the mature protein.

To simplify the protein purification process, a purification tag may be added either at the 5' or 3' end of the gene coding sequence. Commonly used purification tags include a stretch of six histidine residues (U.S. Patent Nos. 5,284,933 and 5,310,663), a streptavidin-affinity tag described by Schmidt and Skerra, *Protein Engineering*, 6:109-122 (1993), a FLAG peptide [Hopp *et al.*, *Biotechnology*, 6:1205-

1210 (1988)], glutathione S-transferase [Smith and Johnson, *Gene*, 67:31-40 (1988)], and thioredoxin [LaVallie *et al.*, *BioTechnology*, 11:187-193 (1993)]. To remove these peptide or polypeptides, a proteolytic cleavage recognition site may be inserted at the fusion junction. Commonly used proteases are factor Xa, thrombin, and enterokinase.

The invention also provides purified and isolated *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* virulence polypeptides encoded by a polynucleotide of the invention. Presently preferred are polypeptides comprising the amino acid sequences encoded by any one of the polynucleotides set out in SEQ ID NOs : 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172 and 174, and species homologs thereof. The invention embraces virulence polypeptides encoded by a DNA selected from the group consisting of : a) the DNA sequence set out in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172, and 174 and species homologs thereof; b) DNA molecules encoding *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica*. polypeptides encoded by any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172, and 174, and species homologs thereof; and c) a DNA molecule, encoding a virulence gene product, that hybridizes under moderately stringent conditions to the DNA of (a) or (b).

The invention also embraces polypeptides that have at least about 99%, at least about 95%, at least about 90%, at least about 85%, at least about 80%, at least about 75%, at least about 70%, at least about 65%, at least about 60%, at least

about 55%, and at least about 50% identity and/or homology to the preferred polypeptides of the invention. Percent amino acid sequence "identity" with respect to the preferred polypeptides of the invention is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in the virulence gene product sequence after aligning both sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Percent sequence "homology" with respect to the preferred polypeptides of the invention is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in one of the virulence polypeptide sequences after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and also considering any conservative substitutions as part of the sequence identity. Conservative substitutions can be defined as set out in Tables A and B.

**Table A**  
**Conservative Substitutions I**

<u>SIDE CHAIN CHARACTERISTIC</u>	<u>AMINO ACID</u>
Aliphatic	Non-polar
	G A P I L V
	Polar - uncharged
	C S T M N Q
	Polar - charged
	D E K R
Aromatic	H F W Y
Other	N Q D E

Polypeptides of the invention may be isolated from natural bacterial cell sources or may be chemically synthesized, but are preferably produced by recombinant procedures involving host cells of the invention. Virulence gene products of the invention may be full length polypeptides, biologically active fragments, or variants thereof which retain specific biological or immunological activity. Variants may comprise virulence polypeptide analogs wherein one or more

of the specified (*i.e.*, naturally encoded) amino acids is deleted or replaced or wherein one or more non-specified amino acids are added: (1) without loss of one or more of the biological activities or immunological characteristics specific for the virulence gene product; or (2) with specific disablement of a particular biological activity of the virulence gene product. Deletion variants contemplated also include fragments lacking portions of the polypeptide not essential for biological activity, and insertion variants include fusion polypeptides in which the wild-type polypeptide or fragment thereof have been fused to another polypeptide.

Variant virulence polypeptides include those wherein conservative substitutions have been introduced by modification of polynucleotides encoding polypeptides of the invention. Conservative substitutions are recognized in the art to classify amino acids according to their related physical properties and can be defined as set out in Table A (from WO 97/09433, page 10, published March 13, 1997 (PCT/GB96/02197, filed 9/6/96). Alternatively, conservative amino acids can be grouped as defined in Lehninger, [Biochemistry, Second Edition; Worth Publishers, Inc. NY:NY (1975), pp.71-77] as set out in Table B.

**Table B**  
**Conservative Substitutions II**

<u>SIDE CHAIN</u>	
<u>CHARACTERISTIC</u>	<u>AMINO ACID</u>
Non-polar (hydrophobic)	
A. Aliphatic:	A L I V P
B. Aromatic:	F W
C. Sulfur-containing:	M
D. Borderline:	G
Uncharged-polar	
A. Hydroxyl:	S T Y
B. Amides:	N Q
C. Sulfhydryl:	C
D. Borderline:	G
Positively Charged (Basic):	K R H
Negatively Charged (Acidic):	D E

Variant virulence products of the invention include mature virulence gene products, *i.e.*, wherein leader or signal sequences are removed, having additional amino terminal residues. Virulence gene products having an additional methionine residue at position -1 are contemplated, as are virulence products having additional methionine and lysine residues at positions -2 and -1. Variants of these types are particularly useful for recombinant protein production in bacterial cell types. Variants of the invention also include gene products wherein amino terminal sequences derived from other proteins have been introduced, as well as variants comprising amino terminal sequences that are not found in naturally occurring proteins.

The invention also embraces variant polypeptides having additional amino acid residues which result from use of specific expression systems. For example, use of commercially available vectors that express a desired polypeptide as a fusion protein with glutathione-S-transferase (GST) provide the desired polypeptide having an additional glycine residue at position -1 following cleavage of the GST component from the desired polypeptide. Variants which result from expression using other vector systems are also contemplated.

Also comprehended by the present invention are antibodies (*e.g.*, monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, humanized, human, and CDR-grafted antibodies, including compounds which include CDR sequences which specifically recognize a polypeptide of the invention) and other binding proteins specific for virulence gene products or fragments thereof. The term "specific for" indicates that the variable regions of the antibodies of the invention recognize and bind a virulence polypeptide exclusively (*i.e.*, are able to distinguish a single virulence polypeptides from related virulence polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see

Harlow *et al.* (Eds), Antibodies A Laboratory Manual; Cold Spring Harbor Laboratory; Cold Spring Harbor, NY (1988), Chapter 6. Antibodies that recognize and bind fragments of the virulence polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as  
5 defined above, a virulence polypeptide of the invention from which the fragment was derived.

The DNA and amino acid sequence information provided by the present invention also makes possible the systematic analysis of the structure and function of the virulence genes and their encoded gene products. Knowledge of a  
10 polynucleotide encoding a virulence gene product of the invention also makes available anti-sense polynucleotides which recognize and hybridize to polynucleotides encoding a virulence polypeptide of the invention. Full length and fragment anti-sense polynucleotides are provided. The worker of ordinary skill will appreciate that fragment anti-sense molecules of the invention include (i) those which  
15 specifically recognize and hybridize to a specific RNA (as determined by sequence comparison of DNA encoding a virulence polypeptide of the invention to DNA encoding other known molecules) as well as (ii) those which recognize and hybridize to RNA encoding variants of the family of virulence proteins. Antisense polynucleotides that hybridize to RNA encoding other members of the virulence  
20 family of proteins are also identifiable through sequence comparison to identify characteristic, or signature, sequences for the family of molecules.

The invention further contemplates methods to modulate gene expression through use of ribozymes. For a review, see Gibson and Shillito, *Mol. Biotech.* 7:125-137 (1997). Ribozyme technology can be utilized to inhibit translation  
25 of mRNA in a sequence specific manner through (i) the hybridization of a complementary RNA to a target mRNA and (ii) cleavage of the hybridized mRNA through nuclease activity inherent to the complementary strand. Ribozymes can be identified by empirical methods but more preferably are specifically designed based on accessible sites on the target mRNA [Bramlage, *et al.*, *Trends in Biotech* 16:434-438 (1998)]. Delivery of ribozymes to target cells can be accomplished using either  
30

exogenous or endogenous delivery techniques well known and routinely practiced in the art. Exogenous delivery methods can include use of targeting liposomes or direct local injection. Endogenous methods include use of viral vectors and non-viral plasmids.

5               Ribozymes can specifically modulate expression of virulence genes when designed to be complementary to regions unique to a polynucleotide encoding a virulence gene product. "Specifically modulate" therefore is intended to mean that ribozymes of the invention recognizes only a single polynucleotide. Similarly, ribozymes can be designed to modulate expression of all or some of a family of  
10           proteins. Ribozymes of this type are designed to recognize polynucleotide sequences conserved in all or some of the polynucleotides which encode the family of proteins.

              The invention further embraces methods to modulate transcription of a virulence gene of the invention through use of oligonucleotide-directed triplet helix formation. For a review, see Lavrovsky, *et al.*, *Biochem. Mol. Med.* 62:11-22 (1997).  
15           Triplet helix formation is accomplished using sequence specific oligonucleotides which hybridize to double stranded DNA in the major groove as defined in the Watson-Crick model. Hybridization of a sequence specific oligonucleotide can thereafter modulate activity of DNA-binding proteins, including, for example, transcription factors and polymerases. Preferred target sequences for hybridization  
20           include transcriptional regulatory regions that modulate virulence gene product expression. Oligonucleotides which are capable of triplet helix formation are also useful for site-specific covalent modification of target DNA sequences. Oligonucleotides useful for covalent modification are coupled to various DNA damaging agents as described in Lavrovsky, *et al.* [*supra*].

25           The identification of *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* virulence genes renders the genes and gene products useful in methods for identifying anti-bacterial agents. Such methods include assaying potential agents for the ability to interfere with expression of virulence gene products represented by the DNA sequences set forth in any one of SEQ ID NOS: 1,  
30           3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68,

70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs thereof (i.e., the genes represented by DNA sequences of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 encode the virulence gene product, or the DNA sequences of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 are adjacent the gene encoding the virulence gene product, or are involved in regulation of expression of the virulence gene product), or assaying potential agents for the ability to interfere with the function of a bacterial gene product encoded in whole or in part by a DNA sequence set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, species homologs thereof, or the complementary strand thereof, followed by identifying agents that are positive in such assays. Polynucleotides and polypeptides useful in these assays include not only the genes and encoded polypeptides as disclosed herein, but also variants thereof that have substantially the same activity as the wild-type genes and polypeptides.

The virulence gene products produced by the methods described above are used in high throughput assays to screen for inhibitory agents. The sources for potential agents to be screened are chemical compound libraries, fermentation media of *Streptomyces*, other bacteria and fungi, and cell extracts of plants and other vegetations. For proteins with known enzymatic activity, assays are established based

on the activity, and a large number of potential agents are screened for ability to inhibit the activity. For proteins that interact with another protein or nucleic acid, binding assays are established to measure such interaction directly, and the potential agents are screened for ability to inhibit the binding interaction.

5                   The use of different assays known in the art is contemplated according to this aspect of the invention. When the function of the virulence gene product is known or predicted by sequence similarity to a known gene product, potential inhibitors can be screened in enzymatic or other types of biological and/or biochemical assays keyed to the function and/or properties of the gene product. When  
10 the virulence gene product is known or predicted by sequence similarity to a known gene product to interact with another protein or nucleic acid, inhibitors of the interaction can be screened directly in binding assays. The invention contemplates a multitude of assays to screen and identify inhibitors of binding by the virulence gene product. In one example, the virulence gene product is immobilized and interaction  
15 with a binding partner is assessed in the presence and absence of a putative inhibitor compound. In another example, interaction between the virulence gene product and its binding partner is assessed in a solution assay, both in the presence and absence of a putative inhibitor compound. In both assays, an inhibitor is identified as a compound that decreases binding between the virulence gene product and its binding  
20 partner. Other assays are also contemplated in those instances wherein the virulence gene product binding partner is a protein. For example, variations of the di-hybrid assay are contemplated wherein an inhibitor of protein/protein interactions is identified by detection of a positive signal in a transformed or transfected host cell as described in PCT publication number WO 95/20652, published August 3, 1995.

25                   Candidate inhibitors contemplated by the invention include compounds selected from libraries of potential inhibitors. There are a number of different libraries used for the identification of small molecule modulators, including: (1) chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules. Chemical  
30 libraries consist of structural analogs of known compounds or compounds that are

identified as "hits" or "leads" via natural product screening. Natural product libraries are collections of microorganisms, animals, plants, or marine organisms which are used to create mixtures for screening by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of plants or marine organisms. Natural product libraries include polyketides, non-ribosomal peptides, and variants (non-naturally occurring) thereof. For a review, see *Science* 282:63-68 (1998). Combinatorial libraries are composed of large numbers of peptides, oligonucleotides, or organic compounds as a mixture. They are relatively easy to prepare by traditional automated synthesis methods, PCR, cloning, or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to modulate activity.

Still other candidate inhibitors contemplated by the invention can be designed and include soluble forms of binding partners, as well as binding partners as chimeric, or fusion, proteins. Binding partners as used herein broadly encompasses antibodies, antibody fragments, and modified compounds comprising antibody domains that are immunospecific for the expression product of the identified virulence gene.

Other assays may be used when a binding partner (*i.e.*, ligand) for the virulence gene product is not known, including assays that identify binding partners of the target protein through measuring direct binding of test binding partner to the target protein, and assays that identify binding partners of target proteins through affinity ultrafiltration with ion spray mass spectroscopy/HPLC methods or other physical and analytical methods. Alternatively, such binding interactions are evaluated indirectly using the yeast two-hybrid system described in Fields and Song, *Nature*, 340:245-246 (1989), and Fields and Sternglanz, *Trends in Genetics*, 10:286-292 (1994), both of

which are incorporated herein by reference. The two-hybrid system is a genetic assay for detecting interactions between two proteins or polypeptides. It can be used to identify proteins that bind to a known protein of interest, or to delineate domains or residues critical for an interaction. Variations on this methodology have been developed to clone genes that encode DNA-binding proteins, to identify peptides that bind to a protein, and to screen for drugs. The two-hybrid system exploits the ability of a pair of interacting proteins to bring a transcription activation domain into close proximity with a DNA-binding domain that binds to an upstream activation sequence (UAS) of a reporter gene, and is generally performed in yeast. The assay requires the construction of two hybrid genes encoding (1) a DNA-binding domain that is fused to a first protein and (2) an activation domain fused to a second protein. The DNA-binding domain targets the first hybrid protein to the UAS of the reporter gene; however, because most proteins lack an activation domain, this DNA-binding hybrid protein does not activate transcription of the reporter gene. The second hybrid protein, which contains the activation domain, cannot by itself activate expression of the reporter gene because it does not bind the UAS. However, when both hybrid proteins are present, the noncovalent interaction of the first and second proteins tethers the activation domain to the UAS, activating transcription of the reporter gene. When the virulence gene product (the first protein, for example) is already known to interact with another protein or nucleic acid, this assay can be used to detect agents that interfere with the binding interaction. Expression of the reporter gene is monitored as different test agents are added to the system; the presence of an inhibitory agent results in lack of a reporter signal.

When the function of the virulence gene product is unknown and no ligands are known to bind the gene product, the yeast two-hybrid assay can also be used to identify proteins that bind to the gene product. In an assay to identify proteins that bind to the first protein (the target protein), a large number of hybrid genes each encoding different second proteins are produced and screened in the assay. Typically, the second protein is encoded by a pool of plasmids in which total cDNA or genomic DNA is ligated to the activation domain. This system is applicable to a wide variety

of proteins, and it is not even necessary to know the identity or function of the second binding protein. The system is highly sensitive and can detect interactions not revealed by other methods; even transient interactions may trigger transcription to produce a stable mRNA that can be repeatedly translated to yield the reporter protein.

5 Other assays may be used to search for agents that bind to the target protein. One such screening method to identify direct binding of test ligands to a target protein is described in U.S. Patent No. 5,585,277, incorporated herein by reference. This method relies on the principle that proteins generally exist as a mixture of folded and unfolded states, and continually alternate between the two  
10 states. When a test ligand binds to the folded form of a target protein (i.e., when the test ligand is a ligand of the target protein), the target protein molecule bound by the ligand remains in its folded state. Thus, the folded target protein is present to a greater extent in the presence of a test ligand which binds the target protein, than in the absence of a ligand. Binding of the ligand to the target protein can be determined  
15 by any method which distinguishes between the folded and unfolded states of the target protein. The function of the target protein need not be known in order for this assay to be performed. Virtually any agent can be assessed by this method as a test ligand, including, but not limited to, metals, polypeptides, proteins, lipids, polysaccharides, polynucleotides and small organic molecules.

20 Another method for identifying ligands for a target protein is described in Wieboldt *et al.*, *Anal. Chem.*, 69:1683-1691 (1997), incorporated herein by reference. This technique screens combinatorial libraries of 20-30 agents at a time in solution phase for binding to the target protein. Agents that bind to the target protein are separated from other library components by centrifugal ultrafiltration. The  
25 specifically selected molecules that are retained on the filter are subsequently liberated from the target protein and analyzed by HPLC and pneumatically assisted electrospray (ion spray) ionization mass spectroscopy. This procedure selects library components with the greatest affinity for the target protein, and is particularly useful for small molecule libraries.

The inhibitors/binders identified by the initial screens are evaluated for their effect on virulence in *in vivo* mouse models of *P. multocida* infections. Models of bacteremia, endocarditis, septic arthritis, soft tissue abscess, or pneumonia may be utilized. Models involving use of other animals are also comprehended by the invention. For example, rabbits can be challenged with a wild type *P. multocida* strain before or after administration of varying amounts of a putative inhibitor/binder compound. Control animals, administered only saline instead of putative inhibitor/binder compound provide a standard by which deterioration of the test animal can be determined. Other animal models include those described in the Animal and Plant Health Inspection Service, USDA, January 1, 1994 Edition, §§113.69-113.70; Panciera and Corstvet, *Am. J. Vet. Res.* 45:2532-2537; Ames, *et al.*, *Can. J. Comp. Med.* 49:395-400 (1984); and Mukkur, *Infection and Immunity* 18:583-585 (1977). Inhibitors/binders that interfere with bacterial virulence are can prevent the establishment of an infection or reverse the outcome of an infection once it is established.

Any adjuvant known in the art may be used in the vaccine composition, including oil-based adjuvants such as Freund's Complete Adjuvant and Freund's Incomplete Adjuvant, mycolate-based adjuvants (*e.g.*, trehalose dimycolate), bacterial lipopolysaccharide (LPS), peptidoglycans (*i.e.*, mureins, mucopeptides, or glycoproteins such as N-Opaca, muramyl dipeptide [MDP], or MDP analogs), proteoglycans (*e.g.*, extracted from *Klebsiella pneumoniae*), streptococcal preparations (*e.g.*, OK432), Biostim™ (*e.g.*, 01K2), the "Iscoms" of EP 109 942, EP 180 564 and EP 231 039, aluminum hydroxide, saponin, DEAE-dextran, neutral oils (such as miglyol), vegetable oils (such as arachis oil), liposomes, Pluronic® polyols, the Ribi adjuvant system (see, for example GB-A-2 189 141), or interleukins, particularly those that stimulate cell mediated immunity. An alternative adjuvant consisting of extracts of *Amycolata*, a bacterial genus in the order Actinomycetales, has been described in U.S. Patent No. 4,877,612. Additionally, proprietary adjuvant mixtures are commercially available. The adjuvant used will depend, in part, on the

recipient organism. The amount of adjuvant to administer will depend on the type and size of animal. Optimal dosages may be readily determined by routine methods.

The vaccine compositions optionally may include vaccine-compatible pharmaceutically acceptable (*i.e.*, sterile and non-toxic) liquid, semisolid, or solid diluents that serve as pharmaceutical vehicles, excipients, or media. Any diluent known in the art may be used. Exemplary diluents include, but are not limited to, polyoxyethylene sorbitan monolaurate, magnesium stearate, methyl- and propylhydroxybenzoate, talc, alginates, starches, lactose, sucrose, dextrose, sorbitol, mannitol, gum acacia, calcium phosphate, mineral oil, cocoa butter, and oil of theobroma.

The vaccine compositions can be packaged in forms convenient for delivery. The compositions can be enclosed within a capsule, caplet, sachet, cachet, gelatin, paper, or other container. These delivery forms are preferred when compatible with entry of the immunogenic composition into the recipient organism and, particularly, when the immunogenic composition is being delivered in unit dose form. The dosage units can be packaged, *e.g.*, in tablets, capsules, suppositories or cachets.

The vaccine compositions may be introduced into the subject to be immunized by any conventional method including, *e.g.*, by intravenous, intradermal, intramuscular, intramammary, intraperitoneal, or subcutaneous injection; by oral, sublingual, nasal, anal, or vaginal, delivery. The treatment may consist of a single dose or a plurality of doses over a period of time.

The invention also comprehends use of an attenuated bacterial strain of the invention for manufacture of a vaccine medicament to prevent or alleviate bacterial infection and/or symptoms associated therewith. The invention also provides use of inhibitors of the invention for manufacture of a medicament to prevent or alleviate bacterial infection and/or symptoms associated therewith.

The present invention is illustrated by the following examples. Example 1 describes constructions of *P. multocida* mutants. Example 2 relates to screening for *P. multocida* mutants. Example 3 addresses methods to determine

virulence of the *P. multocida* mutants. Example 4 describes cloning of *P. multocida* virulence genes. Example 5 addresses identification of genes in other species related to *P. multocida* virulence genes. Example 6 describes construction of *A. pleuropneumoniae* mutants. Example 7 addresses screening for attenuated *A. pleuropneumoniae* mutants. Example 8 relates to identification of *A. pleuropneumoniae* virulence genes. Example 9 describes competition challenge of *A. pleuropneumoniae* mutants and wild type bacteria. Example 10 characterizes *A. pleuropneumoniae* genes identified. Example 11 addresses efficacy of *A. pleuropneumoniae* mutant to protect against wild type bacterial challenge. Example 12 describes identification of species homolog virulence genes in *P. (Mannheimia) haemolytica*.

#### Example 1

##### Construction of a Library of Tagged-Transposon *P. multocida* Mutants

A library of tagged-transposon mutants was constructed in parental vector pLOF/Km [Herrero, *et al.*, *J Bacteriol.* 172:6557-67 (1990)] which has previously been demonstrated to be functional and random in *P. multocida* [Lee, *et al.*, *Vet Microbiol.* 50:143-8 (1996)]. Plasmid pLOF/Km was constructed as a modification of suicide vector pGP704 and included a transposase gene under control of the *Tac* promoter as well as the mini-Tn10 transposable element encoding kanamycin resistance. Plasmid pTEF-1 was constructed as described below by modifying pLOF/Km to accept sequence tags which contained a semi-random [NK]<sub>35</sub> sequence.

Plasmid pLOF/Km was first modified to eliminate the unique *Kpn*I restriction site in the multiple cloning region and then to introduce a new *Kpn*I site in the mini-Tn10 region. The plasmid was digested with *Kpn*I and the resulting overhanging ends were filled in with Klenow polymerase according to manufacturer's suggested protocol. Restriction digests and ligations described herein were performed according to manufacturer's suggested protocols (Gibco BRL, Gaithersburg, MD and Boehringer Mannheim, Indianapolis, IN). The blunt end product was self-ligated to

produce a plasmid designated pLOF/Km--*KpnI* which was transformed into *E.coli* DH5 $\alpha$ : $\lambda$ pir for amplification. *E.coli* DH5 $\alpha$ : ( $\lambda$ pir  $\phi$ 80dlacZ $\Delta$ M15, recA1, endA1, gyrA96, thi-1, hsdR17(r<sub>k</sub><sup>-</sup>, m<sub>k</sub><sup>-</sup>, supE44, relA1, deoR,  $\Delta$ (lacZYA-argF)U169, was propagated at 37°C in Luria-Bertani (LB) medium. Plasmids were prepared using

5 QIAGEN SpinPreps from QIAGEN Inc. (Santa Clarita, CA) and digested with *SfiI* which cuts at a unique site within the mini-Tn10 transposable element. A *SfiI*-*KpnI*-*SfiI* adaptor was prepared by annealing oligonucleotides TEF1 (SEQ ID NO: 86) and TEF3 (SEQ ID NO: 87) and the resulting double-stranded adapter was ligated into the *SfiI* site to create plasmid pTEF-1. Oligonucleotides TEF1 and TEF3 (as well as all

10 other oligonucleotides described herein) were synthesized by Genosys Biotechnologies (The Woodlands, TX).

TEF1 5'-AGGCCGGTACCGGCCGCTT SEQ ID NO: 86

15 TEF3 5'-CGGCCGGTACCGGCCTAGG SEQ ID NO: 87

Unique sequence tags for insertion into the *KpnI* site of pTEF-1 were prepared as follows. PCR was carried out to generate double stranded DNA tags using a GeneAmp XL PCR Kit (PE Applied Biosystems, Foster City, CA) under

20 conditions including 250  $\mu$ M each dNTP, 1.5 mM Mg(OAc)<sub>2</sub>, 100 pmol each primer TEF14 (SEQ ID NO: 88) and TEF15 (SEQ ID NO: 89), 1 ng TEF26 (SEQ ID NO: 90) as template DNA and 2.5 units recombinant *Tth* DNA Polymerase XL.

TEF14 5'-CATGGTACCCATTCTAAC SEQ ID NO: 88

25

TEF15 5'-CTAGGTACCTACAACCTC SEQ ID NO: 89

TEF26 SEQ ID NO: 90

5'-CTAGGTACCTACAACCTCAAGCTT-[NK]<sub>35</sub>-

30

AAGCTTGGTTAGAAATGGGTACCATG

Reaction conditions included an initial incubation at 95°C for one minute, followed by thirty cycles of 30 seconds at 95°C, 45 seconds at 45°C, and 15 seconds at 72°C, followed by a final incubation at 72°C for two minutes. The PCR products were digested with *KpnI* and purified using a QIAGEN Nucleotide Removal Kit (QIAGEN, Inc., Chatsworth, GA) according to the manufacturer's suggested protocol. The unique tag sequences were ligated into the mini-Tn10 element of linearized pTEF-1, previously digested with *KpnI* and dephosphorylated with calf intestinal alkaline phosphatase (Boehringer Mannheim) using standard procedures. The resulting plasmid library was transformed into *E.coli* DH5 $\alpha$ : $\lambda$ pir. Colony blot analysis was performed according to the DIG User's Guide (Boehringer-Mannheim) with hybridization and detection performed as follows.

Hybridizations were essentially performed according to the Genius Non-Radioactive User's Guide (Boehringer Mannheim Biochemicals), the product sheet for the DIG-PCR labeling kit (Boehringer Mannheim Biochemicals), and the product sheet for CSPD (Boehringer Mannheim Biochemicals). For preparation of probes, a 100  $\mu$ l primary PCR reaction was set up using Amplitaq PCR buffer (PE Applied Biosystems), 200  $\mu$ M dNTPs, 140 pmol each of primers TEF5 (SEQ ID NO: 91) and TEF6 (SEQ ID NO: 92), 2 mM MgCl<sub>2</sub>, 2.5 units Amplitaq (PE Applied Biosystems) and 1 ng of plasmid DNA.

TEF5      5'-TACCTACAACCTCAAGCT      SEQ ID NO: 91

TEF6      5'-TACCCATTCTAACCAAGC      SEQ ID NO: 92

Cycle conditions included an initial incubation at 95°C for two minutes, followed by 35 cycles of 95°C for 30 seconds, 50°C for 45 seconds, 72°C for 15 seconds and a final incubation at 72°C for three minutes. The amplification products were separated using electrophoresis on a 2% - 3:1 NuSieve GTG (FMC BioProducts, Rockland, ME, USA):Agarose gel and the 109 bp product was excised and purified. Gel extractions were carried out using a QIAGEN Gel Extraction kit (QIAGEN).

Approximately 15 ng of the primary product was labeled in a 50 µl PCR reaction using the DIG PCR Kit, 50 pmol each of primers TEF24 and TEF25, and a 1:1 mix of DIG Probe Synthesis Mix with 2 mM dNTP stock solution.

5                    TEF24        5'-TACCTACAACCTCAAGCTT        SEQ ID NO: 93

                  TEF25        5'-TACCCATTCTAACCAAGCTT        SEQ ID NO: 94

10                    PCR conditions included an initial incubation at 95°C for four minutes, followed by 25 cycles of 95°C for 30 seconds, 50°C for 45 seconds, 72°C for 15 seconds and a final incubation at 72°C for three minutes. The labeled PCR product was digested with *Hind*III in a total reaction volume of 90 µl and purified from the constant primer arms using a 2% - 3:1 NuSieve GTG (FMC BioProducts):Agarose gel. The region containing the labeled variable tag was excised and the entire gel slice was dissolved

15                    and denatured in 10 ml of DIG EasyHyb at 95°C for ten minutes.

                  Dot blots were prepared using a Hybond<sup>®</sup>-N<sup>+</sup> membrane (Amersham-Pharmacia Biotech). Target DNA for each tag was prepared in 96 well plates using approximately 30 ng of PCR product. An equal volume of 0.1 N NaOH was added to denature the sample and each sample was applied to the membrane with minimal

20                    vacuum using a Minifold I<sup>™</sup> Dot-Blot Apparatus from Schleicher and Schuell (Keene, NH, USA). Each well was washed with 150 µl of Neutralization Solution (0.5 M Tris /3 M NaCl, pH 7.5) and 150 µl of 2X SSC. Membranes were UV-crosslinked in a Stratalink (Stratagene, La Jolla, CA, USA) and prehybridized for one hour in 20 mls DIG EasyHyb Buffer at 42°C. The denatured probe was added and

25                    hybridization carried out overnight at 42°C. The membrane was washed two times in 2X SSC containing 0.1% SDS for five minutes each wash. Two high stringency washes were performed in 50 ml of pre-warmed 0.1X SSC buffer containing 0.1% SDS at 68°C for 15 minutes before proceeding with standard Genius Detection protocols (Genius Manual ).

It is desirable to use a non-radioactive detection system for safety, lower cost, ease of use, and reduction of hazardous materials. In initial experiments using similar procedures previously described [Mei, *et al.*, *Mol Microbiol.* 26:399-407 (1997)], unacceptable background levels of hybridization were obtained in negative controls. In order to decrease background, tag length was increased by 30 bp to a total of 70, amplification primers were lengthened to include all sequence flanking the variable region, a lower concentration of dig-dUTP was used, and the conserved sequences flanking the sequence tag region were removed by gel purification. Most significantly, PCR was used to generate [NK]<sub>33</sub> sequence tags as the target DNA in dot blots rather than the entire plasmids containing the tagged transposons after detecting background hybridization from the transposon itself. Using these modifications background was eliminated making chemiluminescent/non-radioactive screening more effective.

Approximately four hundred different transformants resulting from the ligation of pTEF-1 with the PCR generated sequence tags were screened by colony blot and the 96 strongest hybridizing colonies were assembled into microtiter plates for further use. Even though the likelihood of duplicated tags was very low, half of the plate of master tags was probed against the other to confirm that no tags were duplicated. The plasmids containing these tags were purified and transformed into *E.coli* S17-1:λpir (pir, *recA*, *thi*, *pro*, *hsd*, (r-m+), RP4-2, (Tc::Mu), (Km::Tn7), [TmpR], [SmR]), and the transformed bacteria propagated at 37°C in Luria-Bertani (LB) medium. Each of the 96 *E.coli* S17-1:λpir transformants containing the tagged plasmid pTEF-1 was used in conjugative matings to generate transposon mutants of *P. multocida*. *P. multocida* strain TF5 is a spontaneous nalidixic acid resistant mutant derived from UC6731, a bovine clinical isolate. *P. multocida* strains were grown on brain heart infusion (BHI) media (Difco Laboratories, Detroit, MI, USA) at 37°C and in 5% CO<sub>2</sub> when grown on plates. Matings were set up by growing each *E.coli* S17-1:λpir/pTEF1:[NK]<sub>33</sub> clone and the TF5 strain to late log phase. Fifty μl of culture for each tagged-pTEF-1 clone was mixed with 200 μl of the TF5 culture and 50 μl of each mating mixture was spotted onto 0.22 TM filters previously placed on BHI plates

containing 100 mM IPTG and 10 mM MgSO<sub>4</sub>. Following overnight incubation at 37°C with 5% CO<sub>2</sub>, mating mixtures were washed off of each filter into 3 ml of PBS and 25 µl of each was plated onto BHIN<sup>50</sup>K<sup>100</sup> plates. Following selective overnight growth, colonies were assembled into microtiter plates by toothpick transfer into 200 µl BHIN<sup>50</sup>K<sup>50</sup> making sure that each well in a microtiter plate always contained a transposon mutant with the same sequence tag. Following overnight growth, 50 µl of 75% glycerol was added to each well and plates were stored frozen at -80°C.

Nineteen pools were assembled by transferring the transposon mutants to microtiter plates making sure that each well contained a transposon mutant with the appropriate tag for that well. In other words, a specific well in each microtiter plate always contained a transposon mutant with the same sequence tag even though the location of the transposon within those mutants may be different.

## Example 2

### Murine Screening for Attenuated *P. multocida* Mutants

Nineteen pools of *Pasteurella multocida* transposon mutants were screened using a murine model of septicemia. Frozen plates of pooled *P. multocida* transposon mutants were removed from -80°C storage and subcultured by transferring 10 µl from each well to a new 96 well round bottom plate (Corning Costar, Cambridge, MA, USA) containing 200 µl of brain heart infusion (DIFCO) with 50 µg/ml nalidixic acid (Sigma) and 50 µg/ml kanamycin (Sigma) (BHIN<sup>50</sup>K<sup>50</sup>). Plates were incubated without shaking overnight at 37°C in 5% CO<sub>2</sub>. Overnight plates were subcultured by transferring 10 µl from each well to a new flat bottomed 96-well plate (Corning Costar) containing 100 µl of BHI per well and incubating at 37°C with shaking at approximately 150 rpm. The OD<sub>540</sub> was monitored using a micro-titer plate reader. At an OD<sub>540</sub> of approximately 0.2 to 0.25, each plate was pooled to form the "input pool" by combining 100 µl from each of the wells of the micro-titer plate. The culture was diluted appropriately in BHI to doses of approximately 10<sup>4</sup>, 10<sup>5</sup>, 10<sup>6</sup> CFU/ml and 0.2 ml of each dilution was used to infect female 14-16 g BALB/c mice by intraperitoneal administration. At two days post-infection, one or two surviving mice were euthanized and the spleens harvested. The entire spleen was homogenized

in 1.0 ml sterile 0.9 % saline. Dilutions of the homogenate from  $10^{-2}$  to  $10^{-5}$  were prepared and plated onto BHI<sup>50</sup>K<sup>50</sup> plates. Following overnight growth, at least 20,000 colonies were pooled in 10 mls BHI broth to form the "recovered pool" and 0.5 ml of the recovered pool was centrifuged at 3,500 X g and the pellet used to  
5 prepare genomic DNA according to a previously described protocol [Wilson, *In F. M. Ausubel, et al.*(ed.), Current Protocols in Molecular Biology, vol. 1. John Wiley and Sons, New York, p. 2.4.1-2.4.5. (1997)].

Initial experiments with virulent wild-type *P. multocida* indicated that organisms could be recovered from the spleen, lungs, kidneys, and liver indicating a truly septicemic model of infection. Dot blots for both the "input" and "recovered" pools were performed as described in Example 1 and evaluated both by visual  
10 inspection and by semi-quantitative analysis. Hybridization was carried out as described in Example 1 except that 5 µg of genomic DNA from input and recovered pools was used as template. Semi-quantitative analysis indicates whether a significant reduction in a single clone has occurred. If a mutant is unable to survive within the host, then the recovered signal should be very low compared to the input signal yielding a high input/recovered ratio. Most mutants will grow as well *in vivo* as *in vitro* and therefore a ratio of their signals should be approximately equal to 1. Clones selected by quantitative analysis as being highly reduced in the recovered pool were  
15 selected for further study. Additional clones with questionable input/recovered ratios were also selected after visually evaluating films made from the dot blots.  
20

### Example 3

#### Determination of Virulence for *P. multocida* Candidate Mutants

Each potential mutant which exhibited reduced recovery from splenic tissue was isolated from the original pool plate and used individually in a challenge experiment to verify and roughly estimate the attenuation caused by the transposon mutation. Individual candidate mutants from *in vivo* screens were grown on Sheep Blood Agar plates overnight in 5% CO<sub>2</sub> at 37°C. Approximately six colonies of each  
25 mutant were inoculated into BHI broth and allowed to grow for six hours. Dilutions were prepared and five mice each were infected as described above with  $10^2$ ,  $10^3$ ,  $10^4$   
30

and  $10^3$  CFU each. Attenuation was determined by comparing mortality after six days relative to the wild type. Surviving mice were presumed to be protected and then challenged with a dose of wild type *P. multocida* at a concentration approximately 200-fold greater than the  $LD_{50}$  for the wild type strain. Survival rate was then determined for each challenged group of mice.

Results indicated that 62 of 120 potential transposon mutants were attenuated, having an approximate  $LD_{50}$  of at least 10 fold higher than the wild type strain. The clones and their approximate  $LD_{50}$  values are listed in Table 1. A control experiment with the wild type strain was run in parallel with each set of challenges and in all cases mortality in wild type-challenged groups was 100%.

In addition to  $LD_{50}$  values, Table 1 also provides data from vaccination and challenge experiments. Briefly, groups of mice ( $n = 5$  to 10) were vaccinated by intraperitoneal injection with the individual *P. multocida* strains shown in Table 1 at a dose that was approximately 200 times greater than the  $LD_{50}$  of the virulent, wild type strain. Animals were observed for 28 days after which mortality figures were calculated.

**Table 1**  
***P. multocida* Virulence Genes**

Nucleotide SEQ ID NO:	Representative Isolate	PossibleGene Function	Vaccination # survivors/total	Challenge # survivors/total	$LD_{50}$
-	wild type	-	0/0	-	<10
23	PM1B1	guaB	10/10, 10/10, 10/10	9/10, 9/10	4.3 x 106
11	PM1D1	dstB	10/10, 5/10	10/10, 5/5	8.4 x 104
3	PM1BD7	atpG	5/5, 10/10	10/10	>3 x 105
74	PM1BE11	yhjJ (HI0145)	10/10	5/10	>2 x 105
70	PM1BF6	yabK (HI1020)	3/5, 8/10	9/9	>2 x 105
19	PM2G8	flaC	4/5, 9/10	9/9	>4 x 105
76	PM3C9	yiaO (HI0146)	3/5		>6 x 105
118	PM3G11	UnkO	4/5, 10/10	10/10	>3 x 105
31	PM7B4	iroA (UnkB)	0/5		
17	PM4C6	flaB (flaB2)	2/5, 10/10, 9/10	10/10, 9/9	>3 x 106
9	PM4G10-T9	dnaA	4/5		>5 x 105
1	PM4D5-T5	atpB	5/5		>4 x 105
53	PM4D5-T1	UnkC2	5/5		>4 x 105
15	PM4F2	flaB (flaB1)	3/5, 6/10, 10/10	6/6, 10/10	>3 x 105
41	PM5F7	rneB	4/5		1 x 103
7	PM5E2	devB	0/5, 3/10	2/3	ND
68	PM6H5-T1	xyzA	5/5		>3 x 105
78	PM6H8	yigF (HI0719)	5/5, 9/10	9/9	>3 x 105
108	PM7D12	pmp	5/5, 9/10	9/9	
51	PM8C1R1-T2	UnkC1	5/5		>6 x 105

Nucleotide SEQ ID NO:	Representative Isolate	Possible Gene Function	Vaccination # survivors/total	Challenge # survivors/total	LD <sub>50</sub>
37	PM8C1-T3	mgIB	5/5		~6 x 10 <sup>5</sup>
58	PM8C1R1-T6	UnkD1	5/5		~6 x 10 <sup>5</sup>
43	PM10H7	purF (H11707)	3/5, 8/10, 8/10	8/8, 8/8	>3 x 10 <sup>5</sup>
23	PM10H10-T2	H11501	5/5		>1 x 10 <sup>4</sup>
72	PM11G8-T2	ygiK	5/5		>2.4 x 10 <sup>3</sup>
21	PM11G8-T4	greA	5/5		>2.4 x 10 <sup>3</sup>
84	PM12H6	yyam (H10687)	3/5, 0/10		~2.2 x 10 <sup>3</sup>
33	PM15G8-T2	kdtB	5/5		>1.2 x 10 <sup>5</sup>
116	PM15G8-T1	UnkK	5/5		>1.2 x 10 <sup>5</sup>
104	PM16G11-T1	hmbR	3/5		>1.9 x 10 <sup>5</sup>
29	PM16G11-T2	hxaC	3/5		>1.9 x 10 <sup>5</sup>
35	PM16H8	lglC	5/5, 10/10	10/10	>2.4 x 10 <sup>5</sup>
80	PM16H3	yleA (H10019)	5/5, 10/10		>2.0 x 10 <sup>5</sup>
49	PM17H6-T1	sopE	4/5		~6 x 10 <sup>5</sup>
120	PM17H6	UnkP	4/5		~6 x 10 <sup>5</sup>
5	PM18F5-T8	cap5E	5/5		>2.4 x 10 <sup>5</sup>
82	PM18F5-T10	yoyB (H10345)	5/5		>2.4 x 10 <sup>5</sup>
13	PM19A1	exbB	5/5, 10/10	10/10	>1.2 x 10 <sup>5</sup>
112	PM19D4	rci	5/5, 8/10	8/8	~1.6 x 10 <sup>5</sup>
39	PM20A12	mioC (H10669)	3/5, 8/10	8/8	~2 x 10 <sup>4</sup>
60	PM20C2	UnkD2	5/5, 10/10	10/10	>8.2 x 10 <sup>6</sup>

#### Example 4

##### Cloning and Identification of Genes Required for *P. multocida* Virulence

Each transposon mutant which was verified to be attenuated was analyzed further to determine the identity of the disrupted open reading frame. DNA from each mutant was amplified, purified, and digested with restriction enzymes that were known not to cut within the transposon and generally produced 4-8 kb fragments that hybridized with the transposon. Using selection for kanamycin resistance encoded by the transposon, at least one fragment for each transposon mutant was cloned.

Southern hybridization with multiple restriction enzymes was performed for each attenuated mutant using a labeled 1.8 kb *Mlu*I fragment from pLOF/Km as a probe to identify a suitably sized fragment for cloning. The mini-Tn10 element and flanking DNA from each mutant was cloned into pUC19 and the flanking sequence determined using internal primers TEF32 and TEF40, primer walking and in some cases universal pUC-19 primers.

TEF-32 GGCAGAGCATTACGCTGAC SEQ ID NO: 95  
TEF-40 GTACCGGCCAGGCGGCCACGCGTATTC SEQ ID NO:96

Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377 DNA Sequencer. Double stranded sequence for putative interrupted open reading frames was obtained for each clone. Sequencer 3.0 software (Genecodes, Corp., Ann Arbor, MI) was used to assemble and analyze sequence data. GCG programs [Devereux, *et al.*, 1997. Wisconsin Package Version 9.0, 9.0 ed. Genetics Computer Group, Inc., Madison] were used to search for homologous sequences in currently available databases.

In 37% of the clones that were identified as being attenuated, there were multiple insertions of the mini-Tn10 transposable element. Each insertion including its flanking sequence was cloned individually into pGP704 and mated into the wild-type strain to produce new mutants of *P. multocida*, each carrying only one of the multiple original insertions. Individual mutants were retested individually to determine the insertion responsible for the attenuated phenotype. The nucleotide sequence of the disrupted, predicted open reading frame was determined by sequencing both strands, and the predicted amino acid sequence was used to search currently available databases for similar sequences. Sequences either matched known genes, unknown genes, and hypothetical open reading frames previously sequenced or did not match any previously identified sequence. For those genes having homology to previously identified sequences, potential functions were assigned as set out in Table 1.

25

#### Example 5 Identification of Related Genes in Other Species

In separate experiments, STM was also performed using *Actinobacillus pleuropneumoniae* (App). One of the App strains contained an insertion in a gene that was sequenced (SEQ ID NO: 97) and identified as a species homolog of the *P. multocida* *atpG* gene. This result suggested the presence in other bacterial species of

30

homologs to previously unknown *P. multocida* genes that can also be mutated to produce attenuated strains of the other bacterial species for use in vaccine compositions. In order to determine if homologs of other *P. multocida* genes exists in other bacterial species, Southern hybridization was performed on genomic DNA from other species using the *A. pleuropneumoniae atpG* gene as a probe.

*Actinobacillus pleuropneumoniae*, *Pasteurella haemolytica* (Ph), *P. multocida*, and *Haemophilus somnus* (Hs) genomic DNA was isolated using the CTAB method and digested with *EcoRI* and *HindIII* for two hours at 37°C. Digested DNA was separated on a 0.7% agarose gel at 40V in TAE buffer overnight. The gel was immersed sequentially in 0.1 M HCL for 30 minutes, twice in 0.5 M NaOH/1.5 M NaCl for 15 minutes each, and twice in 2.5 M NaCl/1 M Tris, pH 7.5. The DNA was transferred to nitrocellulose membranes (Amersham Hybond N<sup>+</sup>) overnight using 20X SSC buffer (3 M NaCl/0.3 M sodium citrate). The DNA was crosslinked to the membrane using a UV Stratalinker on autocrosslink setting (120 millijoules). The membrane was prehybridized in 5X SSC/ 1% blocking solution/0.1% sodium lauroyl sarcosine/0.02% SDS at 50°C for approximately seven hours and hybridized overnight at 50°C in the same solution containing a PCR generated atgG probe.

The probe was prepared using primers DEL-1389 (SEQ ID NO: 98) and TEF-46 (SEQ ID NO: 99) in a with a GeneAmp XL PCR kit in a GeneAmp PCR System 2400. Template was genomic *A. pleuropneumoniae* DNA.

DEL-1389	TCTCCATTCCCTTGCTGCGGCAGGG	SEQ ID NO: 98
TEF-46	GGAATTACAGCCGGATCCGGG	SEQ ID NO: 99

The PCR was performed with an initial heating step at 94°C for five minutes, 30 cycles of denaturation t 94°C for 30 sec, annealing at 50°C for 30 sec, and elongation at 72°C for three minutes, and a final extension step at 72°C for five minutes. The amplification products were separated on an agarose gel, purified using a QIAquick gel purification kit (QIAGEN), and labeled using a DIG-High Primer kit (Boehringer Mannheim). The blot was removed from the hybridization solution and rinsed in 2X

SSC and washed two times for five minutes each wash in the same buffer. The blot was then washed two times for 15 minutes each in 0.5X SSC at 60°C. Homologous bands were visualized using a DIG Nucleic Acid Detection Kit (Boehringer Mannheim).

- 5 Single bands were detected in *Pasteurella haemolytica*, *Haemophilus somnus* and *A. pleuropneumoniae* using *EcoRI* digested DNA. Two bands were detected using *EcoRI* digested DNA from *Pasteurella multocida*.

### Example 6

#### 10 Construction of a Library of Tagged-Transposon *P. multocida* Mutants

- Transposon mutagenesis using pLOF/Km has previously been reported to be functional and random in *A. pleuropneumoniae* [Tascon, *et al.*, *J Bacteriol.* 175:5717-22 (1993)]. To construct tagged transposon mutants of *A. pleuropneumoniae*, each of 96 *E. coli* S17-1: $\lambda$ pir transformants containing pre-selected tagged plasmids (pTEF-1:[NK]<sub>35</sub>) was used in conjugative matings to generate transposon mutants of *A. pleuropneumoniae* strain AP225, a serotype 1 spontaneous nalidixic acid resistant mutant derived from an in vivo passaged ATCC 27088 strain. *A. pleuropneumoniae* strains were grown on Brain Heart Infusion (BHI) (Difco Laboratories, Detroit, MI) media with 10  $\mu$ g/ml B-nicotinamide adenine dinucleotide (V<sup>10</sup>), (Sigma, St. Louis, Missouri) at 37°C and in 5% CO<sub>2</sub> when grown on plates. *E. coli* S17-1: $\lambda$ pir ( $\lambda$ pir, *recA*, *thi*, *pro*, *hsdR*(r<sub>-</sub>m<sub>+</sub>), RP4-2, (Tc<sup>R</sup>::Mu), (Km<sup>R</sup>::Tn7), [Tm<sup>R</sup>], [Sm<sup>R</sup>]) was propagated at 37°C in Luria-Bertani (LB) medium. Antibiotics when necessary were used at 100  $\mu$ g/ml ampicillin (Sigma), 50  $\mu$ g/ml nalidixic acid (N<sup>50</sup>)(Sigma), and 50 (K<sup>50</sup>) or 100 (K<sup>100</sup>)  $\mu$ g/ml of kanamycin (Sigma).

- 25 Matings were set up by growing each *E. coli* S17-1: $\lambda$ pir/pTEF1:[NK]<sub>35</sub> clone and the AP225 strain to late log phase. A 50  $\mu$ l aliquot of culture for each tagged-pTEF-1 clone was mixed with 150  $\mu$ l of the AP225 culture, and then 50  $\mu$ l of each mating mixture was spotted onto 0.22  $\mu$ M filters previously placed onto BHIV<sup>10</sup> plates containing 100  $\mu$ M IPTG and 10 mM MgSO<sub>4</sub>. Following overnight incubation at 37°C with 5% CO<sub>2</sub>, mating mixtures were washed off of each filter into 2 ml of PBS and 200  $\mu$ l of each was plated onto BHIV<sup>10</sup>N<sup>50</sup>K<sup>100</sup> plates. After selective

overnight growth, colonies were assembled into microtiter plates by toothpick transfer into 200  $\mu$ l BHIV<sup>10</sup>N<sup>30</sup>K<sup>50</sup> making sure that each well in a microtiter plate always contained a transposon mutant with the same sequence tag. Following overnight growth, 50  $\mu$ l of 75% glycerol was added to each well and plates were stored frozen at -80°C.

APP does not appear to have as much bias towards multiple insertions of the mini-Tn10 element as did *P. multocida*. Only approximately 3% of the mutants were determined to contain multiple insertions, which is in agreement with the 4% previously reported [Tascon, *et al.*, *J Bacteriol.* 175:5717-22 (1993)]. A problem in APP consisted of identifying numerous mutants (discussed below) containing insertions into 23S RNA regions: 28 total mutants with insertions into 13 unique sites. This may indicate that 23S RNA contains preferential insertion sites and that the growth of APP is affected by these insertions enough to result in differential survival within the host. Southern blot analysis using an APP 23S RNA probe suggests that APP may contain only three ribosomal operons as compared to five in *H. influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)] and seven complete operons in *E. coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)]. This site preference and its effect on growth rate may be a significant barrier to "saturation mutagenesis" since a significant number of clones will contain insertions into these rRNAs and large volume screening will be necessary to obtain additional unique attenuating mutations.

#### **Example 7** **Porcine Screening for Attenuated *A. pleuropneumoniae* Mutants**

Twenty pools of *A. pleuropneumoniae* transposon mutants, containing a total of approximately 800 mutants, were screened using a porcine intratracheal infection model. Each pool was screened in two separate animals.

Frozen plates of pooled *A. pleuropneumoniae* transposon mutants were removed from -80°C storage and subcultured by transferring 20  $\mu$ l from each well to a new 96 well round bottom plate (Corning Costar, Cambridge, MA, USA) containing 180  $\mu$ l of BHIV<sup>10</sup>N<sup>30</sup>K<sup>50</sup>. Plates were incubated without shaking overnight at 37°C in

5% CO<sub>2</sub>. Overnight plates were then subcultured by transferring 10 µl from each well to a new flat bottomed 96 well plate (Corning Costar) containing 100 µl of BHIV<sup>10</sup> per well and incubating at 37°C with shaking at 150 rpm. The OD<sub>562</sub> was monitored using a microtiter plate reader. At an OD<sub>562</sub> of approximately 0.2 to 0.25, each plate

5 was pooled to form the "input pool" by combining 100 µl from each of the wells of the microtiter plate. The culture was diluted appropriately in BHI to approximately 2 X 10<sup>6</sup> CFU/ml. For each diluted pool, 4.0 ml was used to infect 10-20 kg SPF pigs (Whiteshire-Hamroc, Albion, IN) by intratracheal administration using a tracheal tube. At approximately 20 hours post-infection, all surviving animals were euthanized and

10 the lungs removed. Lavage was performed to recover surviving bacteria by infusing 150 mls of sterile PBS into the lungs, which were then massaged to distribute the fluid. The lavage fluid was recovered, and the process was repeated a second time. The lavage fluid was centrifuged at 450 x g for 10 minutes to separate out large debris. Supernatants were then centrifuged at 2,800 x g to pellet the bacteria. Pellets

15 were resuspended in 5 mls BHI and plated in dilutions ranging from 10<sup>-2</sup> to 10<sup>-5</sup> onto BHIV<sup>10</sup>N<sup>150</sup>K<sup>50</sup> plates. Following overnight growth, at least 100,000 colonies were pooled in 10 mls BHI broth to form the "recovered pools". A 0.7 ml portion of each recovered pool was used to prepare genomic DNA by the CTAB method [Wilson, *In* Ausubel, *et al.*, (eds.), Current Protocols in Molecular Biology, vol. 1. John Wiley and

20 Sons, New York, p. 2.4.1-2.4.5 (1997)].

Recovery from the animals routinely was in the 10<sup>8</sup> CFU range from lung lavage.

Dot blots were performed and evaluated both by visual inspection and by semi-quantitative analysis as described previously. All hybridizations and

25 detections were performed as described. Briefly, probes were prepared by a primary PCR amplification, followed by agarose gel purification of the desired product and secondary PCR amplification incorporating dig-dUTP. Oligonucleotides including TEF5, TEF6, TEF24, TEF25, TEF48 and TEF62, were synthesized by Genosys Biotechnologies (The Woodlands, TX). Primers TEF69, TEF65, and TEF66 were also

30 used for inverse PCR reactions and sequencing.



Table 2 shows the *A. pleuropneumoniae* genes identified and extent to which open reading frames were determinable. Sequence identification numbers are provided for nucleotide sequences as well as deduced amino acid sequences where located.

**Table 2**  
***A. pleuropneumoniae* Open Reading Frames**

<u>Complete Open Reading Frame</u>		<u>NO Start Codon - Stop Codon</u>	
atpH	SEQ ID NO: 134	dksA	SEQ ID NO: 136
aptG	SEQ ID NO: 132	dnaK	SEQ ID NO: 138
exbB	SEQ ID NO: 140	HI0379	SEQ ID NO: 144
OmpP5	SEQ ID NO: 152		
OmpP5-2	SEQ ID NO: 150	<u>NO Start Codon - NO Stop Codon</u>	
tig	SEQ ID NO: 160	pnp	SEQ ID NO: 154
fkpA	SEQ ID NO: 142	apvA-or 1	SEQ ID NO: 122
hupA	SEQ ID NO: 146	apvA-or 2	SEQ ID NO: 124
rpmF	SEQ ID NO: 158	apvB	SEQ ID NO: 126
		apvD	SEQ ID NO: 130
<u>Start Codon - NO Stop Codon</u>		<u>RNA or Noncoding Sequences</u>	
lpdA	SEQ ID NO: 148	tRNA-leu	SEQ ID NO: 162
potD	SEQ ID NO: 156	tRNA-glu	SEQ ID NO: 163
yaeE	SEQ ID NO: 164		
apvC	SEQ ID NO: 128		

The putative identities listed in Table 3 (below, Example 9) were assigned by comparison with bacterial databases. The 110 mutants represented 35 groups of unique transposon insertions. The number of different mutations per loci varied, with some clones always containing an insertion at a single site within an ORF to clones containing insertions within different sites of the same ORF. Three multiple insertions were detected in the 110 mutants screened as determined by production of multiple PCR bands and generation of multiple sequence electropherograms.

**Example 9**  
**Competition Challenge of *A. pleuropneumoniae***  
**Mutants with Wild Type APP225**

A representative clone from each of the unique attenuated mutant groups identified above that was absent or highly reduced in the recovered population was isolated from the original pool plate and used in a competition challenge experiment with the wild type strain (AP225) to verify the relative attenuation caused by the transposon mutation. Mutant and wild type strains were grown in BHIV<sup>10</sup> to an OD<sub>590</sub> of 0.6 -- 0.9. Approximately 5.0 x 10<sup>6</sup> CFU each of the wild type and mutant strains were added to 4 mls BHI. The total 4 ml dose was used infect a 10-20 kg SPF pig by intratracheal administration with a tracheal tube. At approximately 20 hours post-infection, all surviving animals were euthanized and the lungs removed. Lung lavages were performed as described above. Plate counts were carried out on BHIV<sup>10</sup>N<sup>50</sup> and BHIV<sup>10</sup>N<sup>50</sup>K<sup>100</sup> to determine the relative numbers of wild type to mutant in both the input cultures and in the lung lavage samples. A Competitive Index (CI) was calculated as the  $[\text{mutant CFU} / \text{wild type CFU}]_{\text{input}} / [\text{mutant CFU} / \text{wild type CFU}]_{\text{recovered}}$ .

Of the 35 potential transposon mutants, 22 were significantly attenuated, having a competitive index (CI) of less than 0.2. A transposon mutant that did not seem to be attenuated based on the STM screening results was chosen from one of the pools as a positive control. This mutant had a CI in vivo of approximately 0.6. An in vitro competition was also done for this mutant resulting in a CI of 0.8. The mutant was subsequently determined to contain an insertion between 2 phenylalanine tRNA's.

Competitive indices for unique attenuated single-insertion mutants are listed in Table 3. Competitive indices for *atpG*, *pnp*, and *exbB* App mutants indicated that the mutants were unable to compete effectively with the wild type strains and were therefore attenuated.

**Table 3**  
**Virulence and Proposed Function of *A. pleuropneumoniae* Mutants**

Mutant	Similarity	Putative or Known Functions	C.I.
AP20A6	<i>atpH</i>	ATP synthase	.009
AP7F10	<i>atpG</i>	ATP synthase	.013
AP17C6	<i>lpdA</i>	dihydrolipoamide dehydrogenase	.039
AP11E7	<i>exbB</i>	transport of iron compounds	.003, .003, .006
AP3H7	<i>potD</i>	Spermidine/putrescine transport	.308
AP8H6	<i>OmpP5</i>	Adhesin / OmpA homolog	.184
AP18H8	<i>OmpP5-2</i>	Adhesin / OmpA homolog	.552
AP13E9	<i>tlg</i>	Peptidyl-prolyl isomerase	.050
AP13C2	<i>flpA</i>	Peptidyl-prolyl isomerase	<.001
AP15C11	<i>pnp</i>	Polynucleotide phosphorylase	.032
AP18F12	<i>hupA</i>	Histone – like protein	.001
AP20F8	<i>dksA</i>	Dosage dependent suppressor of dnaK mutations	.075
AP5G4	<i>dnaK</i>	Heat shock protein – molecular chaperone	.376
AP17C9	<i>tRNA-leu</i>	Protein Synthesis	.059
AP5D6	<i>tRNA-glu</i>	Protein Synthesis	.055
AP18B2	<i>rpmF</i>	Protein Synthesis	.112
AP10E7	<i>yaeA</i>	Unknown	.001
AP19A5	HI0379	Unknown	.061
AP10C10	<i>apvA</i>	Unknown	.157
AP18F5	<i>apvB</i>	Unknown	.103
AP2A6	<i>apvC</i>	Unknown	.091
AP2C11	<i>apvD</i>	Unknown	.014

Accuracy of the CI appeared to be very good as the *exbB* mutant was competed within three different animals yielding CI's of 0.003, 0.003 and 0.006. The use of a Competitive Index number to assign attenuation based upon one competition in a large animal study was further confirmed based on preliminary vaccination results in pigs with 7 mutants (n=8) described below in Example 11.

### Example 10

#### Characterization of Attenuated *A. pleuropneumoniae* Virulence Genes

The *A. pleuropneumoniae* genes identified represent four broad functional classes: biosynthetic enzymes, cellular transport components, cellular regulation components and unknowns.

The *atpG* gene, encoding the F<sub>1</sub>- $\gamma$  subunit of the F<sub>0</sub>F<sub>1</sub> H<sup>+</sup>-ATPase complex, can function in production of ATP or in the transport of protons by hydrolyzing ATP. A related *atpG* attenuated mutant was also identified in *P. multocida*. Another *atp* gene, *atpH*, that encodes the F<sub>1</sub>  $\delta$  subunit was also identified. Phenotypes of *atp* mutants include non-adaptable acid-sensitivity phenotype [Foster, *J Bacteriol.* 173:6896-6902 (1991)], loss of virulence in *Salmonella typhimurium* [Garcia del Portillo, *et al.*, *Infect Immun.* 61:4489-4492 (1993)] and *P. multocida* (above) and a reduction in both transformation frequencies and induction of competence regulatory genes in *Haemophilus influenzae* Rd [Gwinn, *et al.*, *J Bacteriol.* 179:7315-20 (1997)].

LpdA is a dihydrolipoamide dehydrogenase that is a component of two enzymatic complexes: pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase. While the relationship to virulence is unknown, production of LpdA is induced in *Salmonella typhimurium* when exposed to a bactericidal protein from human which may suggest that this induction may be involved in attempts to repair the outer membrane [Qi, *et al.*, *Mol Microbiol.* 17:523-31 (1995)].

Transport of scarce compounds necessary for growth and survival are critical in vivo. ExbB is a part of the TonB transport complex [Hantke, and Zimmerman, *Microbiology Letters.* 49:31-35 (1981)], interacting with TonB in at least two distinct ways [Karlsson, *et al.*, *Mol Microbiol.* 8:389-96 (1993), Karlsson, *et al.*, *Mol Microbiol.* 8:379-88 (1993)]. Iron acquisition is essential for pathogens. In this work, attenuated *exbB* mutants in both APP and *P. multocida* have been identified. Several TonB-dependent iron receptors have been identified in other bacteria [Biswas, *et al.*, *Mol. Microbiol.* 24:169-179 (1997), Braun, *FEMS Microbiol Rev.* 16:295-307 (1995), Elkins, *et al.*, *Infect Immun.* 66:151-160 (1998), Occhino, *et*

*al.*, *Mol Microbiol.* 29:1493-507 (1998), Stojiljkovic and Srinivasan, *J Bacteriol.* 179:805-12 (1997)]. *A. pleuropneumoniae* produces 2 transferrin-binding proteins, which likely depend on the ExbB/ExbD/TonB system, for acquisition of iron. PotD is a periplasmic binding protein that is required for spermidine (a polyamine) transport [Kashiwagi, *et al.*, *J Biol Chem.* 268:19358-63 (1993)]. Another member of the *Pasteurellaceae* family, *Pasteurella haemolytica*, contains a homologue of *potD* (Lpp38) that is a major immunogen in convalescent or outer membrane protein vaccinated calves [Pandher and Murphy, *Vet Microbiol.* 51:331-41 (1996)]. In *P. haemolytica*, PotD appeared to be associated with both the inner and outer membranes. The role of PotD in virulence or in relationship to protective antibodies is unknown although previous work has shown *potD* mutants of *Streptococcus pneumoniae* to be attenuated [Polissi, *et al.*, *Infect. Immun.* 66:5620-9 (1998)].

Relatively few "classical virulence factors," such as adhesins or toxins with the exception of homologues to OMP P5 of *Haemophilus influenzae*, were identified. *H. influenzae* OMP P5 is a major outer membrane protein that is related to the OmpA porin family of proteins [Munson, *et al.*, *M Infect Immun.* 61:4017-20 (1993)]. OMP P5 in nontypeable *Haemophilus influenzae* has been shown to encode a fimbrial subunit protein expressed as a filamentous structure [Sirakova, *et al.*, *Infect Immun.* 62:2002-20 (1994)] that contributes to virulence and binding of both mucin and epithelial cells [Miyamoto and Bakaletz, *Microb Pathog.* 21:343-56 (1996), Reddy, *et al.*, *Infect Immun.* 64:1477-9 (1996), Sirakova, *et al.*, *Infect Immun.* 62:2002-20 (1994)]. A significant finding was identification of two distinct ORFs that appear to encode OMP P5 homologues. This is also the case with two very similar proteins, MOMP and OmpA2 from *Haemophilus ducreyi*. It remains to be determined whether both are functionally involved in the production of fimbriae and whether the presence of two such ORFs represents a divergent duplication with redundant or complementing functions. Interestingly, the two OMP P5 mutants seem to have disparate CI values, suggesting a difference in essentiality or functionality for only one copy. OMP P5 has been shown to undergo molecular variation during chronic infections [Duim, *et al.*, *Infect Immun.* 65:1351-1356 (1997)], however, this

appears to be restricted to a single gene undergoing point mutations resulting in amino acid changes rather than "type switching" due to differential expression of multiple genes.

Protein folding enzymes are important accessories for the efficient  
5 folding of periplasmic and extracellular proteins, and two genes were identified whose products have peptidyl-prolyl isomerase activity: *fkpA* and *tig* (trigger factor). FkpA is a periplasmic protein that is a member of the FK506-binding protein family [Horne and Young, *Arch Microbiol.* 163:357-65 (1995); Missiakas, *et al.*, *Mol Microbiol.* 21:871-84 (1996)]. FkpA has been shown to contribute to intracellular survival of  
10 *Salmonella typhimurium* [Horne, *et al.*, *Infect Immun.* 65:806-10 (1997)] and a *Legionella pneumophila* homolog, *mip* [Engleberg, *et al.*, *Infect Immun.* 57:1263-1270 (1989)], is responsible for virulence and infection of macrophages [Cianciotto, *et al.*, *J. Infect. Dis.* 162:121-6 (1990); Cianciotto, *et al.*, *Infect. Immun.* 57:1255-1262 (1989)]. Tig, or trigger factor [Crooke and Wickner, *Proc. Natl. Acad. Sci. USA.* 84:5216-20 (1987), Guthrie, and Wickner, *J. Bacteriol.* 172:5555-62 (1990), reviewed  
15 in Hesterkamp, and Bukau., *FEBS Lett.* 389:32-4 (1996)], is a peptidyl prolyl isomerase containing a typical FKBP region [Callebaut and Mornon, *FEBS Lett.* 374:211-215 (1995)], but is unaffected by FK506 [Stoller, *et al.*, *EMBO J.* 14:4939-48 (1995)]. Tig has been shown to associate with the ribosomes and nascent polypeptide chains [Hesterkamp, *et al.*, *Proc Natl Acad Sci USA* 93:4437-41 (1996), Stoller, *et al.*,  
20 *EMBO J.* 14:4939-48 (1995)]. Possible roles include an unknown influence on cell division [Guthrie, and Wickner, *J. Bacteriol.* 172:5555-62 (1990)] in *E. coli*, a role in the secretion and activation of the *Streptococcus pyogenes* cysteine proteinase [Lyon, *et al.*, *EMBO J.* 17:6263-75 (1998)] and survival under starvation conditions in  
25 *Bacillus subtilis* [Gothel, *et al.*, *Biochemistry* 37:13392-9 (1998)].

Bacterial pathogens employ many mechanisms to coordinately regulate gene expression in order to survive a wide variety of environmental conditions within the host. Differences in mRNA stability can modulate gene expression in prokaryotes [Belasco and Higgins, *Gene* 72:15-23 (1988)]. For example, *rnr* (*vacB*) is required  
30 for expression of plasmid borne virulence genes in *Shigella flexneri* [Tobe, *et al.*, *J*

*Bacteriol.* 174:6359-67 (1992)] and encodes the RnaseR ribonuclease [Cheng, *et al.*, *J. Biol. Chem.* 273:14077-14080 (1998)]. PNP is a polynucleotide phosphorylase that is involved in the degradation of mRNA. Null *pnp* / *rnr* mutants are lethal, suggesting a probable overlap of function. It therefore is possible that both *rnr* and *pnp* are involved in the regulation of virulence gene expression. A *pnp* mutant of *P. multocida* is avirulent in a mouse septicemic model (Example 2)]. Other *pnp*-associated phenotypes include competence deficiency and cold sensitivity in *Bacillus subtilis* [Wang and Bechhofer, *J Bacteriol.* 178:2375-82 (1996)].

HupA is a bacterial histone-like protein, which in combination with HupB constitute the HU protein in *E. coli*. Reports have suggested that *hupA* and *hupB* single mutants do not demonstrate any observable phenotype [Huisman, *et al.*, *J Bacteriol.* 171:3704-12 (1989), Wada, *et al.*, *J Mol Biol.* 204:581-91 (1988)], however, *hupA-hupB* double mutants have been shown to be cold sensitive, sensitive to heat shock and blocked in many forms of site-specific DNA recombination [Wada, *et al.*, *J Mol Biol.* 204:581-91 (1988), Wada, *et al.*, *Gene.* 76:345-52 (1989)]. One limited data previously indicated that *hupA* is directly involved in virulence [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)]. The mechanism of *hupA* attenuation remains unknown.

DnaK is a well known and highly conserved heat shock protein involved in regulatory responses to various stressful environmental changes [reviewed in Lindquist and Craig, *Annu Rev Genet.* 22:631-77 (1988)]. DnaK is also one of the most significantly induced stress proteins in *Yersinia enterocolitica* after being phagocytosed by macrophages [Yamamoto, *et al.*, *Microbiol Immunol.* 38:295-300 (1994)] and a *Brucella suis dnaK* mutant failed to multiply within human macrophage-like cells [Kohler, *et al.*, *Mol Microbiol.* 20:701-12 (1996)]. In contrast, another intracellular pathogen, *Listeria monocytogenes*, did not show induction of *dnaK* after phagocytosis [Hanawa, *et al.*, *Infect Immun.* 63:4595-9 (1995)]. A *dnaK* mutant of *Vibrio cholera* affected the production of ToxR and its regulated virulence factors in vitro but similar results were not obtained from in vivo grown cells [Chakrabarti, *et al.*, *Infect Immun.* 67:1025-1033 (1999)]. The CI of *A.*

*pleuropneumonia dnaK* mutant was higher than most of the attenuated mutants although still approximately half of the positive control strain.

DksA is a dosage dependent suppressor of filamentous and temperature-sensitive growth in a *dnaK* mutant of *E. coli* [Kang and Craig, *J Bacteriol.* 172:2055-64 (1990)]. There is currently no defined molecular function for DksA, but the gene has been identified as being critical for the virulence of *Salmonella typhimurium* in chickens and newly hatched chicks [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)]. In that work, it was noted that the *dksA* mutant did not grow well with glucose or histidine but did grow well with glutamine or glutamate as the sole carbon source. This observation may indicate that the *dksA* mutant is somehow impaired in the biosynthesis of glutamate [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)].

Three genes were identified that have roles in protein synthesis: tRNA-leu, tRNA-glu and *rpmF*. Excluding protein synthesis, tRNA's also have a wide variety of functional roles in peptidoglycan synthesis [Stewart, *et al.*, *Nature* 230:36-38 (1971)], porphyrin ring synthesis [Jahn, *et al.*, *Trends Biochem Sci.* 17:215-8 (1992)], targeting of proteins for degradation [Tobias, *et al.*, *Science* 254:1374-7 (1991)], post-translational addition of amino acids to proteins [Leibowitz and Soffer, *B.B.R.C.* 36:47-53 (1969)] and mediation of bacterial-eukaryotic interactions [Gray, *et al.*, *J Bacteriol.* 174:1086-98 (1992), Hromockyj, *et al.*, *Mol Microbiol.* 6:2113-24 (1992)]. More specifically, tRNA-leu is implicated in transcription attenuation [Carter, *et al.*, *Proc. Natl. Acad. Sci. USA* 83:8127-8131 (1986)], lesion formation by *Pseudomonas syringae* [Rich and Willis, *J Bacteriol.* 179:2247-58 (1997)] and virulence of uropathogenic *E. coli* [Dobrindt, *et al.*, *FEMS Microbiol Lett.* 162:135-141 (1998), Ritter, *et al.*, *Mol Microbiol.* 17:109-21 (1995)]. It is unknown whether the tRNA that we have identified represents a minor species of tRNA-leu in *A. pleuropneumoniae*. Regardless, it is possible that tRNA-leu may have any one of a wide range of functions. RpmF is a ribosomal protein whose gene is also part of an operon containing fatty acid biosynthesis enzymes in *E. coli*. Further work will be required to indicate if this is the case in *A. pleuropneumoniae*, although the same

clustering of *fab* genes and *rpmF* occurs in *Haemophilus influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)]. The expression of the *fab* genes is not necessarily dependent on transcripts originating upstream of *rpmF* as there has been a secondary promoter identified within *rpmF* [Zhang and Cronan, Jr., *J Bacteriol.* 180:3295-303 (1998)].

The final class of attenuated mutants includes mutations within genes of unknown function or genes that have not been previously identified. Homologs of *yaeA* and HI0379 have previously been identified in *Escherichia coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)] and *Haemophilus influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)], respectively. The remaining unknowns have been designated *Actinobacillus pleuropneumoniae* virulence genes (*apv*). The *apvC* gene shows significant similarity to HI0893, however, the proposed similarity of HI0893 as a transcriptional repressor similar to the fatty acid response regulator Bm3R1 [Palmer, *J Biol Chem.* 273:18109-16 (1998)] is doubtful. The *apvD* gene is also most similar to a putative membrane protein (b0878) with unknown function from *E. coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)]. Two other unknowns, *apvA* and *apvB* had no significant matches in the public databases.

#### Example 11

##### Safety and Efficacy of *A. pleuropneumoniae* Mutants

Nine groups (n=8) of SPF pigs (4-5 weeks old, 3-10 kg) were used to determine the safety and efficacy of seven *A. pleuropneumoniae* mutants as live attenuated vaccine strains. Seven groups were infected intranasally with  $10^{10}$  CFU of each mutant on day 1. One group was vaccinated on days 1 and 15 with the commercially available vaccine Pleuromune (Bayer), and one naive group was not vaccinated. On day 29, all groups were challenged intranasally with  $1.5 \times 10^5$  CFU per pig of wild type APP225. All surviving animals were euthanized and necropsied on day 42 of the study. Results are shown in Table 4.

**Table 4**  
**Efficacy of *A. pleuropneumoniae* Mutants**

		% Mortality following intranasal challenge	
<u>Vaccine</u>		<u>Vaccination</u>	<u>Challenge</u>
5	Pleuromune	0	37.5
	exbB	0	0
	tig	12.5	0
	fkpA	12.5	0
	HI0385	50.0	0
10	pnp	0	0
	yaeE	0	0
	atpG	0	0
	None	N/A	50.0

15                   The *exbB*, *atpG*, *pnp*, and *yaeA* mutants caused no mortality when administered at a dosage of  $10^{10}$  CFU intranasally. The *fkpA* and *tig* mutant groups had one death each and the HI0379 group (highest CI of the 7 mutants tested shown in Example 9) had four deaths. Wildtype LD<sub>50</sub> using this model was generally  $1 \times 10^7$  CFU, indicating that each of these mutants is at least 100 fold attenuated and that

20                   there is a reasonable correlation between CI and attenuation.

#### **Example 12** **Identification of *P. (Mannheimia) haemolytica* Species Homologs**

25                   Based on the sequences of virulence genes identified in *P. multocida* and *A. pleuropneumoniae*, attempt were made to identify related genes, i.e., species homologs, in *P. (Mannheimia) haemolytica*. PCR was utilized with the degenerate primers shown below to attempt amplification of the *P. (Mannheimia) haemolytica* genes as indicated. Primer sequences, synthesized by Sigma-Genosys (The Woodlands, TX), include standard single letter designations, wherein B indicates

either (C,G or T), D indicates either (G,A or T), H indicates either (A,C or T), K indicates either (G or T), M indicates either (A or C), N indicates either (A,G,C or T), R indicates either (A or G), S indicates either (G or C), V indicates either (G, A, or C), W indicates either (A or T), and Y indicates either (C or T).

5

atpG	TEF146	ATG GCN GGN GCN AAR GAR AT	SEQ ID NO: 176
	TEF148	GCN GCY TTC ATN GCN ACC AT	SEQ ID NO: 177

10

guaB	TEF240	GGN TTY ATY CAY AAA AAY ATG	SEQ ID NO: 178
	TEF243	TCT TTN GTR ATN GTN ACA TCR TG	SEQ ID NO: 179

pnP	TEF141	GCS GGY AAA CCR CGT TGG GAT TGG	SEQ ID NO: 180
	TEF142	CRC CTA ARA TRT CTG AAA GCA CCA C	SEQ ID NO: 181

15

purF	TEF244	ATG TGY GGN ATY GTN GGN AT	SEQ ID NO: 182
	TEF247	CAT ATC AAT ACC ATA CAC ATT	SEQ ID NO: 183

yjgF	TEF162	GGN CCN TAY GTN CAR G	SEQ ID NO: 184
	TEF163	NGC NAC YTC NAC RCA	SEQ ID NO: 185

20

For amplification of initial degenerate PCR products, a 50 µl reaction was set up using 3.3X XL buffer II (PE Applied Biosystems), 200 µM dNTPs, 25 pmol each of the appropriate primers, 0.8 mM MgCl<sub>2</sub>, 0.5 U *rTth* DNA polymerase, XL (PE Applied Biosystems) and approximately 1 µg of TFI DNA.

25

Cycle conditions were 94°C for 1.5 min; followed by 35 cycles of 94°C for 15 s, 40-60°C for 60 s, 72°C for 1.5 min; and a final hold at 72°C for 5 min. Each PCR product was band purified from an agarose gel using the QIAGEN Gel Extraction Kit (QIAGEN, Valencia CA).

30

Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377 DNA Sequencer. Double stranded sequence for the open reading frame (ORF) for each clone was obtained. Sequencher 3.0 software (Genecodes, Corp., Ann Arbor, MI) was used to assemble and analyze sequence data. GCG programs were used to confirm the identity of the ORF by searching for homologous sequences in currently available databases.

35

The Vectorette Kit (Genosys Biotechnologies, The Woodlands, TX) was used to obtain additional flanking sequence for each of the genes. Vectorette libraries were prepared according to the manufacturer's suggested protocol. Perkin Elmer Applied Biosystems GeneAmp XL PCR Kit components were used to create the

5 Vectorette PCR products with the following reaction conditions. A 50  $\mu$ l reaction was set up using 3.3X XL buffer II (PE Applied Biosystems), 200  $\mu$ M dNTPs, 25 pmol each of the appropriate primers (shown below), 0.8 mM MgCl<sub>2</sub>, 0.5 U *rTth* DNA polymerase, XL (PE Applied Biosystems) and 1  $\mu$ l of the appropriate vectorette library. Cycle

10 conditions were 94°C for 1.5 min; followed by 35 cycles of 94°C for 20 s, 60°C for 45s, 72°C for 4 min; and a final hold of 72°C for 7 min. The second primer for each library was the manufacturer's vectorette primer.

Table 5

Gene	Vectorette library	Primer(s)
5	atpG	BglII, HindIII
		TEF217 GAAGCCGCCATACGCTCTTGGG SEQ ID NO: 186
		ClaI
		TEF218 GTTGCTTCCTTTGCCTGCACTGG SEQ ID NO: 187
10	guaB	EcoRI
		TEF265 GGCTCAGAAACAATACCACITTTCA SEQ ID NO: 188
		HindIII, TaqI
		TEF268 GCACCAAAGCAGAATTGTCC SEQ ID NO: 189
15	pnp	ClaI, HincII
		TEF219 GGTGATGATGTCGATGATAGTCCC SEQ ID NO: 190
		TaqI,
		TEF220 GGCGTATTAGCCGTGATGCCAACC SEQ ID NO: 191
		BamHI
20		TEF286 GACCACTTAGGCGATATGGACTT SEQ ID NO: 192
	purF	TaqI
		TEF271 ACCATCATAAAATCGCCTGATTC SEQ ID NO: 193
		TEF292 ACCTGCGGCATCTTGTCTC SEQ ID NO: 194
25		HincII
		TEF274 ACGGGTTTATTTGCCTCTG SEQ ID NO: 195
	yjgF	ClaI
		TEF221 CGCCGGTTTCAGGATTCACGGG SEQ ID NO: 196
30		EcorV
		TEF281 CTGAACAACGTGAAAGCCAT SEQ ID NO: 197

Vectorette PCR products were band purified and sequenced as described above.

Polynucleotide sequences for the *atpG*, *guaB*, *pnp*, *purF*, and *yjgF* genes are set out in SEQ ID NOs: 166, 168, 170, 172 and 174, respectively. Polypeptides encoded by these genes are set out in SEQ ID NOs: 167, 169, 171, 173, and 175, respectively.

;

Numerous modifications and variations in the invention as set forth in the above illustrative examples are expected to occur to those skilled in the art. Consequently only such limitations as appear in the appended claims should be placed on the invention.

## WHAT IS CLAIMED IS:

1. A gram-negative bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104, 108, 112, 116, 118, 120, 122, 124, 126, 128, and 130, or species homologs thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.
2. The gram-negative bacteria of claim 1 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.
3. The gram-negative bacteria of claim 1 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.
4. The gram-negative bacteria of claim 1 wherein said mutation results in deletion of all or part of said gene.
5. An attenuated *Pasteurellaceae* bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172 and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.
6. The *Pasteurellaceae* bacteria of claim 5 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.
7. The *Pasteurellaceae* bacteria of claim 5 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

8. The *Pasteurellaceae* bacteria of claim 5 wherein said mutation results in deletion of all or part of said gene.

9. The *Pasteurellaceae* bacteria of claim 5 selected from the group consisting of *Pasteurella (Mannheimia) haemolytica*, *Pasteurella multocida*, *Actinobacillus pleuropneumoniae* and *Haemophilus somnus*.

10. The *Pasteurellaceae* bacteria of claim 9 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

11. The *Pasteurellaceae* bacteria of claim 9 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

12. The *Pasteurellaceae* bacteria of claim 9 wherein said mutation results in deletion of all or part of said gene.

13. The attenuated *Pasteurellaceae* bacteria of claim 9 that is a *P. multocida* bacteria.

14. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

15. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

16. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in deletion of all or part of said gene.

17. The attenuated *Pasteurellaceae* bacteria of claim 9 that is a *A. pleuropneumoniae* bacteria.

18. The *Pasteurellaceae* bacteria of claim 17 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

19. The *Pasteurellaceae* bacteria of claim 17 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

20. The *Pasteurellaceae* bacteria of claim 17 wherein said mutation results in deletion of all or part of said gene.

21. An immunogenic composition comprising the bacteria according to any one of claims 1 through 20.

22. A vaccine composition comprising the immunogenic composition according to claim 21 and a pharmaceutically acceptable carrier.

23. The vaccine composition according to claim 22 further comprising an adjuvant.

24. A method for producing a gram-negative bacteria mutant comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

25. A method for producing an attenuated *Pasteurellaceae* bacteria comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29,

31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

26. A purified and isolated *Pasteurellaceae* polynucleotide comprising a nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172 and 174.

27. A purified and isolated *Pasteurellaceae* polynucleotide comprising a nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104, 108, 112, 116, 118, 120, 122, 124, 126, 128, and 130.

28. A purified and isolated polynucleotide encoding a *Pasteurellaceae* virulence gene product, or species homolog thereof, selected from the group consisting of:

- a) the polynucleotide according to claim 27,
- b) polynucleotides encoding a polypeptide encoded by the polynucleotide of (a), and
- c) polynucleotides that hybridize to the complement of the polynucleotides of (a) or (b) under moderate stringency conditions.

29. A purified and isolated *Pasteurellaceae* polynucleotide encoding a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOs: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109,

111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175.

30. The polynucleotide of claim 29 which is a DNA.

31. A vector comprising the DNA of claim 30.

32. The vector of claim 31 that is an expression vector, wherein the DNA is operatively linked to an expression control DNA sequence.

33. A host cell stably transformed or transfected with the DNA of claim 30 in a manner allowing the expression of the encoded polypeptide in said host cell.

34. A method for producing a recombinant polypeptide comprising culturing the host cell of claim 33 in a nutrient medium and isolating the encoded polypeptide from said host cell or said nutrient medium.

35. A purified polypeptide produced by the method of claim 34.

36. A purified polypeptide comprising a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOs: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175.

37. An antibody that is specifically reactive with the polypeptide of claim 36.

38. The antibody of claim 33 that is a monoclonal antibody.

39. A method of using the monoclonal antibody of claim 39 for identifying a bacteria of claim 1, 5, 9, or 13 comprising the step of contacting an extract of bacteria with said monoclonal antibody and detecting the absence of binding of said monoclonal antibody.

40. A method of identifying an anti-bacterial agent comprising the steps of assaying potential agents for the ability to interfere with expression or activity of gene products represented by the amino acid sequences set forth in any one of SEQ ID NOS: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175 and identifying an agent that interferes with expression or activity of said gene products.

41. A method of identifying an anti-bacterial agent comprising the steps of:

- a) measuring expression or activity of a gene product as set out in SEQ ID NOS: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175;
- b) contacting the gene product in (a) with a test compound
- c) measuring expression or activity of the gene product in the presence of the test compound; and
- d) identifying the test compound as an antibacterial agent when expression or activity of the gene product is decreased in the presence of the test compound as compared to expression or activity in the presence of the test compound.

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Trp His Val His Leu Asp Thr Leu Leu Phe Ser Ile Ile Ser Gly Ala	
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Val Pro Ser Lys Met Gln Cys Phe Val Gln Ile Met Val Asp Trp Ile	
60 65 70	
gat ggg atc gta aaa gaa aat ttc cat ggt cct cgt cat gct gtt gga	473
Asp Gly Ile Val Lys Glu Asn Phe His Gly Pro Arg His Ala Val Gly	
75 80 85	
cca tta gca tta act att ttc tgc tgg gta ttc att atg aat gct atc	521
Pro Leu Ala Leu Thr Ile Phe Cys Trp Val Phe Ile Met Asn Ala Ile	
90 95 100	
gat ttg atc cca gta gat ttc cta cct caa tta gcc cat tta ttt ggt	569
Asp Leu Ile Pro Val Asp Phe Leu Pro Gln Leu Ala His Leu Phe Gly	
105 110 115 120	
att gaa tac tta aga gct gtt cca aca gca gat atc agt gga aca tta	617
Ile Glu Tyr Leu Arg Ala Val Pro Thr Ala Asp Ile Ser Gly Thr Leu	
125 130 135	
ggc tta tca att ggt gtc ttc ttc tta att att ttc tat aca atc aaa	665
Gly Leu Ser Ile Gly Val Phe Phe Leu Ile Ile Phe Tyr Thr Ile Lys	
140 145 150	
tca aaa ggt atg agt ggc ttt gtt aaa gaa tat acg ctt cat cct ttt	713
Ser Lys Gly Met Ser Gly Phe Val Lys Glu Tyr Thr Leu His Pro Phe	
155 160 165	
aat cat cct ttg tta att ccg gtt aac tta gcg ctt gaa tca gtc aca	761
Asn His Pro Leu Leu Ile Pro Val Asn Leu Ala Leu Glu Ser Val Thr	
170 175 180	
tta tta gca aaa cct gtt tct ttg gcg ttc cgt ctt ttc ggg aat atg	809
Leu Leu Ala Lys Pro Val Ser Leu Ala Phe Arg Leu Phe Gly Asn Met	
185 190 195 200	
tat gca ggt gaa ctt atc ttt att ctt att gca gtg atg tac atg gca	857
Tyr Ala Gly Glu Leu Ile Phe Ile Leu Ile Ala Val Met Tyr Met Ala	
205 210 215	
aat aat ttt gca ctt aat tca atg ggt att ttc atg cat ttg gct tgg	905
Asn Asn Phe Ala Leu Asn Ser Met Gly Ile Phe Met His Leu Ala Trp	
220 225 230	
gct att ttc cat att ctt gtg att acc tta caa gca ttt att ttt atg	953
Ala Ile Phe His Ile Leu Val Ile Thr Leu Gln Ala Phe Ile Phe Met	
235 240 245	
atg ctt aca gtg gtt tat ttg agt atg ggt tat aac aaa gca gaa cac	1001
Met Leu Thr Val Val Tyr Leu Ser Met Gly Tyr Asn Lys Ala Glu His	
250 255 260	
taatttttta taaacaaaac cagaccttgg gtctaaattt caatcttatg gagaacatta	1061
tggaacactg taattactac aacaatcatc gcattctgnaa ttntctctgc t	1112

<210> 2  
 <211> 264  
 <212> PRT  
 <213> *Pasteurella multocida*

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 Phe Leu Lys Thr Gly Asp Ser Phe Trp His Val His Leu Asp Thr Leu  
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 Leu Phe Ser Ile Ile Ser Gly Ala Ile Phe Leu Phe Val Phe Ser Lys  
 35 40 45  
 Val Ala Lys Lys Ala Thr Pro Gly Val Pro Ser Lys Met Gln Cys Phe  
 50 55 60  
 Val Glu Ile Met Val Asp Trp Ile Asp Gly Ile Val Lys Glu Asn Phe  
 65 70 75 80  
 His Gly Pro Arg His Ala Val Gly Pro Leu Ala Leu Thr Ile Phe Cys  
 85 90 95  
 Trp Val Phe Ile Met Asn Ala Ile Asp Leu Ile Pro Val Asp Phe Leu  
 100 105 110  
 Pro Gln Leu Ala His Leu Phe Gly Ile Glu Tyr Leu Arg Ala Val Pro  
 115 120 125  
 Thr Ala Asp Ile Ser Gly Thr Leu Gly Leu Ser Ile Gly Val Phe Phe  
 130 135 140  
 Leu Ile Ile Phe Tyr Thr Ile Lys Ser Lys Gly Met Ser Gly Phe Val  
 145 150 155 160  
 Lys Glu Tyr Thr Leu His Pro Phe Asn His Pro Leu Leu Ile Pro Val  
 165 170 175  
 Asn Leu Ala Leu Glu Ser Val Thr Leu Leu Ala Lys Pro Val Ser Leu  
 180 185 190  
 Ala Phe Arg Leu Phe Gly Asn Met Tyr Ala Gly Glu Leu Ile Phe Ile  
 195 200 205  
 Leu Ile Ala Val Met Tyr Met Ala Asn Asn Phe Ala Leu Asn Ser Met  
 210 215 220  
 Gly Ile Phe Met His Leu Ala Trp Ala Ile Phe His Ile Leu Val Ile  
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 Thr Leu Gln Ala Phe Ile Phe Met Met Leu Thr Val Val Tyr Leu Ser  
 245 250 255  
 Met Gly Tyr Asn Lys Ala Glu His  
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<210> 3  
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 <212> DNA  
 <213> *Pasteurella multocida*

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<222> (364) .. (1230)

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acaacaagca ttagtgttat ttgcagtaga gtttgggttac ttagaagaag tggacttaga 180
tcgtattgggt tcatttgaat cagcactttt agagtatgct aaccataact atgctgattt 240
tatgctgtgag ttaacccaat ctggcaatta caatgatgaa attaaagagt cattaaaagg 300
cattttggat agcttcaaag caaacagtcg gtggttaagt aacactttaa atggagagac 360

aaa atg gca ggt gct aaa gag ata aga acc aaa atc gcg agt gta aaa 408
Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys
1 5 10

agt aca caa aaa att act aaa gcg atg gaa atg gtt gct gcc tcg aaa 456
Ser Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys
20 25 30

atg cgt aaa acg caa gaa cgc atg tct tct tca cgc cct tat tca gaa 504
Met Arg Lys Thr Gln Glu Arg Met Ser Ser Ser Arg Pro Tyr Ser Glu
35 40 45

aca ata cgt aac gcg att agc cac gtt tcc aaa gca acg att ggt tac 552
Thr Ile Arg Asn Val Ile Ser His Thr Ser Lys Ala Thr Ile Gly Tyr
50 55 60

aag cat cca ttt tta gtg gat cgc gaa gta aaa aaa gtg ggc atg att 600
Lys His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile
65 70 75

gtt gtg tcc aca gat cgt ggt ctt tgt ggt ggc tta aac gtg aac ttg 648
Val Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Val Asn Leu
80 85 90 95

ttt aaa act gta tta aat gaa atg aaa gaa tgg aaa gaa aaa gat gtt 696
Phe Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val
100 105 110

tcc gtt caa ttg agt tta atc ggt tct aaa tct atc aac ttt ttc caa 744
Ser Val Gln Leu Ser Leu Ile Gly Ser Lys Ser Ile Asn Phe Phe Gln
115 120 125

tct ttg gga att aaa att tta acc caa gat tca ggt att ggt gat act 792
Ser Leu Gly Ile Lys Ile Leu Thr Gln Asp Ser Gly Ile Gly Asp Thr
130 135 140

ccc tct gtt gag cag tta att ggt tca gtc aat tct atg att gat gct 840
Pro Ser Val Glu Gln Leu Ile Gly Ser Val Asn Ser Met Ile Asp Ala
145 150 155

tat aaa aaa ggg gaa gta gat gtt gtg tat tta gtt tat aac aaa ttt 888
Tyr Lys Lys Gly Glu Val Asp Val Val Tyr Leu Val Tyr Asn Lys Phe
160 165 170 175

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att aac acg atg tgc caa aag cca gta ttg gaa aaa tta att cca tta 936
Ile Asn Thr Met Ser Gln Lys Pro Val Leu Glu Lys Leu Ile Pro Leu
180 185 190

cca gaa tta gat aat gat gaa tta gcc gaa aga aaa caa gtt tgg gat 984
Pro Glu Leu Asp Asn Asp Glu Leu Gly Glu Arg Lys Gln Val Trp Asp
195 200 205

tat att tac gaa cct gat gcg aaa gta tta tta gat aat tta ttg gtt 1032
Tyr Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val
210 215 220

cgt tat tta gaa tct cag gtt tat caa gca gca gtt gaa aac ctt gct 1080
Arg Tyr Leu Glu Ser Gln Val Tyr Gln Ala Ala Val Glu Asn Leu Ala
225 230 235

tct gag caa gcc gct cga atg gtc gcc atg aaa gca gca aca gat aac 1128
Ser Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn
240 245 250 255

gca ggt aac tta att aat gag tta cag tta gtc tat aac aaa gct cgt 1176
Ala Gly Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg
260 265 270

caa gca agt att aca aat gaa tta aat gaa att gtt gcc ggt gca gca 1224
Gln Ala Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala
275 280 285

gca att taacaaatag aggatcggtat atggcaactg gaaaaattgt acaaatcatc 1280
Ala Ile

ggtgcggtta ttgacgttga attcccacaa gatgcagtac caaaagtata tgaatgcctta 1340

aatgttgaaa cagggttagt acttgaagtt caacaacaat taggtggtgg tgaagtgcgc 1400

tgtatcgcaa tgggatcatc tgaatggatta aaacgcgggt taagcgtaac aaatacgaat 1460

aaccacaatt ctgttcagtg gggaacgaaa acattgggtc gtatcatgaa cgtattgggt 1520

gaaccaatcg atgagcaagg tgaaatcggt gcagaagaga attggtctat tcaccgtgcg 1580

ccaccaagtt atgaagaaca atctaacagt actgaacttt tagaaacggg aattaaagtt 1640

atcgacttag ttgtccgtt tcgcaaaagg ggtaaagtag gtttattcgg tgggtcgggt 1700

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tactctgtct ttgcgggggt aggtgagcgt acgcgtgaag gtaacgactt ctatcatgag 1820

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gaaggctcgt atgtcttatt ctccgttgat aa 1972

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&lt;210&gt; 4

&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 4

Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Ser

1	5	10	15
Thr Gln Lys	Ile Thr Lys Ala Met	Glu Met Val Ala Ala	Ser Lys Met
	20	25	30
Arg Lys Thr	Gln Glu Arg Met Ser	Ser Ser Arg Pro Tyr	Ser Glu Thr
	35	40	45
Ile Arg Asn Val	Ile Ser His Val Ser Lys Ala Thr	Ile Gly Tyr Lys	
	50	55	60
His Pro Phe Leu Val Asp Arg	Glu Val Lys Lys Val Gly Met Ile Val		
	65	70	75
Val Ser Thr Asp Arg Gly Leu Cys Gly Gly	Leu Asn Val Asn Leu Phe		
	85	90	95
Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val Ser			
	100	105	110
Val Gln Leu Ser Leu Ile Gly Ser Lys Ser Ile Asn Phe Phe Gln Ser			
	115	120	125
Leu Gly Ile Lys Ile Leu Thr Gln Asp Ser Gly Ile Gly Asp Thr Pro			
	130	135	140
Ser Val Glu Gln Leu Ile Gly Ser Val Asn Ser Met Ile Asp Ala Tyr			
	145	150	155
Lys Lys Gly Glu Val Asp Val Val Tyr Leu Val Tyr Asn Lys Phe Ile			
	165	170	175
Asn Thr Met Ser Gln Lys Pro Val Leu Glu Lys Leu Ile Pro Leu Pro			
	180	185	190
Glu Leu Asp Asn Asp Glu Leu Gly Glu Arg Lys Gln Val Trp Asp Tyr			
	195	200	205
Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val Arg			
	210	215	220
Tyr Leu Glu Ser Gln Val Tyr Gln Ala Ala Val Glu Asn Leu Ala Ser			
	225	230	235
Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala			
	245	250	255
Gly Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln			
	260	265	270
Ala Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala			
	275	280	285

Ile

<210> 5  
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&lt;222&gt; (1)..(813)

&lt;220&gt;

&lt;223&gt; cap5E

&lt;400&gt; 5

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 Val Asp Tyr Ile Tyr His Ala Ala Ala Leu Lys Gln Val Pro Ser Cys  
 1 5 10 15

gag ttt tat ccg tta gag gca gtg aaa acc aat att tta ggt acg gca 96  
 Glu Phe Tyr Pro Leu Glu Ala Val Lys Thr Asn Ile Leu Gly Thr Ala  
 20 25 30

aat gtc tta gaa gcc gcc atc caa aac cag ata aaa cgc gtc gtc tgt 144  
 Asn Val Leu Glu Ala Ala Ile Gln Asn Gln Ile Lys Arg Val Val Cys  
 35 40 45

ctt agc aca gat aaa cgc gtg tac cca att aat gcg atg ggc att tct 192  
 Leu Ser Thr Asp Lys Ala Val Tyr Pro Ile Asn Ala Met Gly Ile Ser  
 50 55 60

aaa gca atg atg gaa aaa gtc atc atc gca aaa tcg cgt aac cta gaa 240  
 Lys Ala Met Met Glu Lys Val Ile Ile Ala Lys Ser Arg Asn Leu Glu  
 65 70 75 80

ggc aca cca acg aca atc tgt tgt act cgc tat ggc aat gtc atg gca 288  
 Gly Thr Pro Thr Thr Ile Cys Cys Thr Arg Tyr Gly Asn Val Met Ala  
 85 90 95

tcg cgt ggt tcg gtt atc cca tta ttt gtc gat caa ata cgt caa ggc 336  
 Ser Arg Gly Ser Val Ile Pro Leu Phe Val Asp Gln Ile Arg Gln Gly  
 100 105 110

aag cct ttt act att act gat cct gag atg aca cgc ttt atg atg aca 384  
 Lys Pro Phe Thr Ile Thr Asp Pro Glu Met Thr Arg Phe Met Met Thr  
 115 120 125

ttg gaa gat gct gtg gat tta gtc cta tat gca ttt aaa aat ggt caa 432  
 Leu Glu Asp Ala Val Asp Leu Val Leu Tyr Ala Phe Lys Asn Gly Gln  
 130 135 140

aat ggt gat gtt ttt gta caa aaa gcc ccc gca gca acc att ggt acc 480  
 Asn Gly Asp Val Phe Val Gln Lys Ala Pro Ala Ala Thr Ile Gly Thr  
 145 150 155 160

ctt gcc aaa gca att acc gaa tta tta tct gtc cca aat cac cct att 528  
 Leu Ala Lys Ala Ile Thr Glu Leu Leu Ser Val Pro Asn His Pro Ile  
 165 170 175

tcc att ata ggt acg cgt cat gga gag aaa gca ttc gaa gct tta tta 576  
 Ser Ile Ile Gly Thr Arg His Gly Glu Lys Ala Phe Glu Ala Leu Leu  
 180 185 190

agc cgt gaa gaa atg gtt cat gca att aat gaa ggt aat tat tat cgc 624  
 Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg  
 195 200 205

atc cca gcc gat caa cgc agt tta aat tac agt aaa tat gtc gaa aaa 672  
 Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys  
 210 215 220

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ggg gaa cca aaa att acc gaa gtc acc gac tac aac tca cat aat act 720
Gly Glu Pro Lys Ile Thr Glu Val Thr Asp Tyr Asn Ser His Asn Thr
225                230                235                240

gag cgt ttg act gtc aag gaa atg aag cag tta ctg ctt aaa ctt gaa 768
Glu Arg Leu Thr Val Lys Glu Met Lys Gln Leu Leu Leu Lys Leu Glu
245                250                255

ttc ata cag aaa atg att gag ggt gaa tac atc tca ccg gag gta 813
Phe Ile Gln Lys Met Ile Glu Gly Glu Tyr Ile Ser Pro Glu Val
260                265                270

taaaaaatgaa agtcttagta actggttcaa atggttttat tgcgaaaaat ctgattcagt 873

ctttatctga ggaacaagat attgagattt tatgttatca ccgtaatcc tctgagaaaa 933

cgcttattca tcatgtattg agtgctgatt ggattattca tcttgccggg gcgaatcgtc 993

cacctgaaga acaagaattt atgacatcaa atacacaatt gacggaaaaa atttgccgta 1053

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tacataaaga aaatggtaat ccgatttata tctgccgttt agctaattgc tttggcaaat 1233

ggtcacgacc tcactataac tcggtagtcg ccacattttg ccataactta attcatgatt 1293

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<210> 6
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<212> PRT
<213> Pasteurella multocida

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20          25          30

Asn Val Leu Glu Ala Ala Ile Gln Asn Gln Ile Lys Arg Val Val Cys
35          40          45

Leu Ser Thr Asp Lys Ala Val Tyr Pro Ile Asn Ala Met Gly Ile Ser
50          55          60

Lys Ala Met Met Glu Lys Val Ile Ile Ala Lys Ser Arg Asn Leu Glu
65          70          75          80

Gly Thr Pro Thr Thr Ile Cys Cys Thr Arg Tyr Gly Asn Val Met Ala
85          90          95

Ser Arg Gly Ser Val Ile Pro Leu Phe Val Asp Gln Ile Arg Gln Gly
100         105         110

Lys Pro Phe Thr Ile Thr Asp Pro Glu Met Thr Arg Phe Met Met Thr
115         120         125

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Leu Glu Asp Ala Val Asp Leu Val Leu Tyr Ala Phe Lys Asn Gly Gln  
 130 135 140  
 Asn Gly Asp Val Phe Val Gln Lys Ala Pro Ala Ala Thr Ile Gly Thr  
 145 150 155 160  
 Leu Ala Lys Ala Ile Thr Glu Leu Leu Ser Val Pro Asn His Pro Ile  
 165 170 175  
 Ser Ile Ile Gly Thr Arg His Gly Glu Lys Ala Phe Glu Ala Leu Leu  
 180 185 190  
 Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg  
 195 200 205  
 Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys  
 210 215 220  
 Gly Glu Pro Lys Ile Thr Glu Val Thr Asp Tyr Asn Ser His Asn Thr  
 225 230 235 240  
 Glu Arg Leu Thr Val Lys Glu Met Lys Gln Leu Leu Leu Lys Leu Glu  
 245 250 255  
 Phe Ile Gln Lys Met Ile Glu Gly Glu Tyr Ile Ser Pro Glu Val  
 260 265 270

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 <213> *Pasteurella multocida*

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 cttattaaag aaaggaatat ggggaagctg tgtgcttgc cttaacctga ataaaggctt 540  
 tttatgacag acaacacaga caatgacaaa ctgtatcgct accttttcca agatcgcgcg 600  
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tatccgaaa gtcacaaaa ctgctcggg gaaatgatgg tggcgaccg tttattgacg 720  
gcgacgttaa aatttgaagg ggatattact gttcaagtac aagggtgatgg accattaaaa 780  
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gcatcagggt atttaactta tcgtaaatgt attcctgcac tgtataactt atataaaact 2580

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                Met Asn Thr Ile Ile Phe Asp Ser Ala Gln His Ala Val

gag aaa att gca caa gaa ttg tta gcg tat agc tta gaa ggt cgc cct 4118
Glu Lys Ile Ala Gln Glu Leu Leu Ala Tyr Ser Leu Glu Gly Arg Pro
    15                20                25

gtg cat att tcc tta tcc gga ggc tca acg ccg aaa ttg tta ttt aaa 4166
Val His Ile Ser Leu Ser Gly Gly Ser Thr Pro Lys Leu Leu Phe Lys
    30                35                40                45

act tta gct caa gca ccg tat aac acc gag att caa tgg aaa aat ttg 4214
Thr Leu Ala Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu
    50                55                60

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cat ttt tgg tgg ggc gat gat cgt atg gtg cca cca acc gat cca gaa 4262  
 His Phe Trp Trp Gly Asp Asp Arg Met Val Pro Pro Thr Asp Pro Glu  
 65 70 75

agt aat tac ggc gag gtg caa aaa ttg tta ttc gat cat att cag atc 4310  
 Ser Asn Tyr Gly Glu Val Gln Lys Leu Leu Phe Asp His Ile Gln Ile  
 80 85 90

cct gca gaa aat att cac cgc att cgt ggt gaa gcc ccc gtt gag agt 4358  
 Pro Ala Glu Asn Ile His Arg Ile Arg Gly Glu Ala Pro Val Glu Ser  
 95 100 105

gaa ctt cac cgt ttt gaa caa gcg cta agt gcg gtc att cct ggg caa 4406  
 Glu Leu His Arg Phe Glu Gln Ala Leu Ser Ala Val Ile Pro Gly Gln  
 110 115 120 125

gtt ttt gat tgg att att ttg ggc atg gga acg gac ggg cac acg gcc 4454  
 Val Phe Asp Trp Ile Ile Leu Gly Met Gly Thr Asp Gly His Thr Ala  
 130 135 140

tca tta ttc cgc cat caa acc gat ttt gac gat cct cat ttc gcc gtg 4502  
 Ser Leu Phe Pro His Gln Thr Asp Phe Asp Asp Pro His Phe Ala Val  
 145 150 155

atc gcg aaa cac cct gaa aca ggg caa att cgt att tca aaa aca gcg 4550  
 Ile Ala Lys His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala  
 160 165 170

aaa ttg att gaa caa gca aag cgg gtg acc tat ttg gtg aca ggt agc 4598  
 Lys Leu Ile Glu Gln Ala Lys Arg Val Thr Tyr Leu Val Thr Gly Ser  
 175 180 185

agt aaa gcc gag atc tta aaa gaa att caa act act cgc gca gaa caa 4646  
 Ser Lys Ala Glu Ile Leu Lys Glu Ile Glu Thr Thr Pro Ala Glu Gln  
 190 195 200 205

ctg cct tat cct gct gcg aaa atc aaa gcg aag cat ggg gtg acg gaa 4694  
 Leu Pro Tyr Pro Ala Ala Lys Ile Lys Ala Lys His Gly Val Thr Glu  
 210 215 220

tgg tat ttg gat aag gat gcg gca aaa tta ctg taatgcgtcg tgagattttt 4747  
 Trp Tyr Leu Asp Lys Asp Ala Ala Lys Leu Leu  
 225 230

caacattttt gcaaaagac ttgaaacaaa atagaccata gcgttcgttt tcaacgagtg 4807

ctgaaaatga aggcctctcgt tgaaaatggc gccatttagt gggtaagcgt aaggttcgct 4867

cagacagcgc tatcaaaagg gtaaaagaat gtatcaactc tattttaate caccaaaatc 4927

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&lt;210&gt; 8

&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 8

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 Ser Leu Ser Gly Gly Ser Thr Pro Lys Leu Leu Phe Lys Thr Leu Ala  
 35 40 45  
 Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu His Phe Trp  
 50 55 60  
 Trp Gly Asp Asp Arg Met Val Pro Pro Thr Asp Pro Glu Ser Asn Tyr  
 65 70 75 80  
 Gly Glu Val Gln Lys Leu Leu Phe Asp His Ile Gln Ile Pro Ala Glu  
 85 90 95  
 Asn Ile His Arg Ile Arg Gly Glu Ala Pro Val Glu Ser Glu Leu His  
 100 105 110  
 Arg Phe Glu Gln Ala Leu Ser Ala Val Ile Pro Gly Gln Val Phe Asp  
 115 120 125  
 Trp Ile Ile Leu Gly Met Gly Thr Asp Gly His Thr Ala Ser Leu Phe  
 130 135 140  
 Pro His Gln Thr Asp Phe Asp Asp Pro His Phe Ala Val Ile Ala Lys

145		150		155		160
His Pro Glu Thr	Gly Gln Ile Arg Ile Ser Lys Thr Ala Lys Leu Ile					
	165			170		175
Glu Gln Ala Lys Arg Val Thr Tyr Leu Val Thr Gly Ser Ser Lys Ala						
	180		185			190
Glu Ile Leu Lys Glu Ile Gln Thr Thr Pro Ala Glu Gln Leu Pro Tyr						
	195		200			205
Pro Ala Ala Lys Ile Lys Ala Lys His Gly Val Thr Glu Trp Tyr Leu						
	210		215			220
Asp Lys Asp Ala Ala Lys Leu Leu						
225		230				

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 <213> *Pasteurella multocida*

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 gaagctgcgc accctgatat cgaattatat accgcatcag ttgatagtca cttaaatgaa 180  
 caaggctata ttattccagg tcttggtgat gccggtgata aaatttttgg cactaaataa 240  
 tcccaacaca agcggcatct tatgccgctt ttttccgttc aatttatagc gcttacaatc 300  
 ttaacagctt gaacactata aaatgaaaag ttaattcaga cagagagttg aaacttaaca 360  
 tgacaaatca aaatccccc gttcttctag aacaaaaatca cgcataaaca gccctcgttg 420  
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 ctggagccca agtcccaatt ttcttagcct ctctctttgc ttttattgca ccaattcaat 600  
 atggcgtggc aacatggggc attgctacta ctatgggggg gctgggtgttt actggactgg 660  
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 ccgtggacat ggcattaggt aaaaacagca cttatcaata taacgatgcc gtattcgttt 840  
 cgatggcaac attattgaca acgttaggtg ttgcggtgtt tgctaaaggc atgatgaaat 900  
 taattcctat catgttttgg attgtcgtcg gctatatact ctgcttattc ttaggcttaa 960

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tcaacttaat cttacccaaa gccaaaaaca cccaataga agaaaatcga taagagaaaa 1620

ttaagggtta agtc ttg ctt aac cct tca ttt ttc gtt tat cct tat tct 1670
          Leu Leu Asn Pro Ser Phe Phe Val Tyr Pro Tyr Ser
          1          5          10

cct ttt ttc gat ttt gta ggt tgc ttt ttg tta gaa aat ttc caa tta 1718
Pro Phe Phe Asp Phe Val Gly Cys Phe Leu Leu Glu Asn Phe Gln Leu
          15          20          25

cct ttg cct att cat caa ctg gat gat gaa acg ctg gat aat ttc tat 1766
Pro Leu Pro Ile His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr
          30          35          40

ccc gac aat aat tta ttg ttg ctg aat tgg cta cgc aaa aat ttt act 1814
Pro Asp Asn Asn Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr
          45          50          55          60

tgt cta aca caa caa ttt ttt tat att tgg ggc gag caa agc agt ggt 1862
Cys Leu Thr Gln Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly
          65          70          75

aaa agt cac ctg tta aaa ggc att act cat cat ttt ttc ctt tta cag 1910
Lys Ser His Leu Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln
          80          85          90

cgc ccc gct atc tat gtg ccc tta gaa aaa tcc caa tat ttc tca ccg 1958
Arg Pro Ala Ile Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro
          95          100          105

gcg gta ctg gaa aac tta gaa caa caa caa ttg gtt tgt tta gat aat 2006
Ala Val Leu Glu Asn Leu Glu Gln Gln Gln Leu Val Cys Leu Asp Asn
          110          115          120

tta cag gca att ata ggc aat act gaa tgg gaa tta gcg att ttt gat 2054
Leu Gln Ala Ile Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp
          125          130          135          140

tta ttt aat cgc ata aaa tct gtt gaa aat aca ctg ctt gtg atc agt 2102
Leu Phe Asn Arg Ile Lys Ser Val Glu Asn Thr Leu Leu Val Ile Ser
          145          150          155

gca aat caa tcc cca act gca tta cct gta agt tta cct gac tta gct 2150

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Ala Asn Gln Ser Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala  
 160 165 170

tca cgt tta cgc tgg gga gaa agc tat cag ctg gtc ccc tta aat gat 2198  
 Ser Arg Leu Arg Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp  
 175 180 185

caa caa aaa atc cat gta ttg caa aaa aat gca cat caa cgt ggt atc 2246  
 Gln Gln Lys Ile His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile  
 190 195 200

gaa ctc ccc gat gaa gta gct aat ttt ctt ttg aaa cgc tta gag cgc 2294  
 Glu Leu Pro Asp Glu Val Ala Asn Phe Leu Lys Arg Leu Glu Arg  
 205 210 215 220

gat atg aaa acg tta ttt gaa gca cta agt aaa tta gat aaa gca tca 2342  
 Asp Met Lys Thr Leu Phe Glu Ala Leu Ser Lys Leu Asp Lys Ala Ser  
 225 230 235

tta caa gcc caa cgt aaa tta acg att ccc ttt gta aaa gaa att tta 2390  
 Leu Gln Ala Gln Arg Lys Leu Thr Ile Pro Phe Val Lys Glu Ile Leu  
 240 245 250

aag cta taaaaaaaaa ccacctcttt atcaggtgat cttcttgct ga 2438  
 Lys Leu

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 <213> Pasteurella multocida

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Phe Val Gly Cys Phe Leu Leu Glu Asn Phe Gln Leu Pro Leu Pro Ile  
 20 25 30

His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr Pro Asp Asn Asn  
 35 40 45

Leu Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr Cys Leu Thr Gln  
 50 55 60

Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly Lys Ser His Leu  
 65 70 75 80

Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln Arg Pro Ala Ile  
 85 90 95

Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro Ala Val Leu Glu  
 100 105 110

Asn Leu Glu Gln Gln Gln Leu Val Cys Leu Asp Asn Leu Gln Ala Ile  
 115 120 125

Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp Leu Phe Asn Arg  
 130 135 140

Ile Lys Ser Val Glu Asn Thr Leu Leu Val Ile Ser Ala Asn Gln Ser  
 145 150 155 160

Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala Ser Arg Leu Arg  
 165 170 175

Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp Gln Gln Lys Ile  
 180 185 190

His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile Glu Leu Pro Asp  
 195 200 205

Glu Val Ala Asn Phe Leu Leu Lys Arg Leu Glu Arg Asp Met Lys Thr  
 210 215 220

Leu Phe Glu Ala Leu Ser Lys Leu Asp Lys Ala Ser Leu Gln Ala Gln  
 225 230 235 240

Arg Lys Leu Thr Ile Pro Phe Val Lys Glu Ile Leu Lys Leu  
 245 250

&lt;210&gt; 11

&lt;211&gt; 2060

&lt;212&gt; DNA

<213> *Pasteurella multocida*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (856)..(1389)

&lt;220&gt;

&lt;223&gt; dsbB

&lt;400&gt; 11

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tgcttctttag tggaaaaatt tgggtgtattt ggctatggcg ccaaatggcc acgtaaagta 120

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gtcaccagcg agcatgctat tggtaaaagc ttccaggaat ccttaccctt cacagcattg 360

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attcagtttg tgctggtgc cagtgaacat actcagcttg ctcttttcta tatttttaac 480

ggtttgttat ccgccatttc agataatgtg tttgtggcca cagtttatat caatgaaac 540

aaagcggcat tagaggctgg cttaattgct caaccacaat atgaattact ggcagtagca 600

attaataccg gtaccaatct tccttctggt gcaaccccaa atggccaagc cgcattctta 660

tttttattga cctcatcact ggcaccatta attcgtcttt cttatggtag aatggtttat 720

atggcattgc cttataccat cgtattatcc tgtattgggt tattgactgt ggaatatatt 780

ttgcctggcg caaccaatgt gctcattcaa attggtttat taaaaccaat gtaatgacaa 840

gtaaaaggag gaaac atg cta agc ttt ttt aag aca ctc tca aca aaa cga 891

Met Leu Ser Phe Phe Lys Thr Leu Ser Thr Lys Arg

1 5 10

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agt gca tgg ttt cta ttg ttt agc tca gct tta cta tta gag gct atc 939
Ser Ala Trp Phe Leu Leu Phe Ser Ser Ser Ala Leu Leu Leu Glu Ala Ile
15 20 25

gct ctt tat ttt caa cat ggc atg ggg ctc gcc cct tgt gtc atg tgt 987
Ala Leu Tyr Phe Gln His Gly Met Gly Leu Ala Pro Cys Val Met Cys
30 35 40

att tac gag agg gta gct att ctt ggc att gct ttc tcc ggt tta ttg 1035
Ile Tyr Glu Arg Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu
45 50 55 60

ggg tta ctc tac ccg agt tcg atg ctt ttg cgc ctt gtg gcg tta tta 1083
Gly Leu Leu Tyr Pro Ser Ser Met Leu Leu Arg Leu Val Ala Leu Leu
65 70 75

att ggt tta agc agt gca atc aaa ggc tta atg att agc atc acc cat 1131
Ile Gly Leu Ser Ser Ala Ile Lys Gly Leu Met Ile Ser Ile Thr His
80 85 90

tta gat cta caa ctt tac cct gca cct tgg aaa caa tgt tca gcg gtg 1179
Leu Asp Leu Gln Leu Tyr Pro Ala Pro Trp Lys Gln Cys Ser Ala Val
95 100 105

gca gaa ttt ccc gag act tta ccc tta gat cag tgg ttt cct gca ctc 1227
Ala Glu Phe Pro Glu Thr Leu Pro Leu Asp Gln Trp Phe Pro Ala Leu
110 115 120

ttc ctc cct tca ggc tca tgc agt gaa gta aca tgg caa ttt ctc ggc 1275
Phe Leu Pro Ser Gly Ser Cys Ser Glu Val Thr Trp Gln Phe Leu Gly
125 130 135 140

ttt tct atg gtg caa tgg atc gtc gtc att ttt gca ctc tat acc tta 1323
Phe Ser Met Val Gln Trp Ile Val Val Phe Ala Leu Tyr Thr Leu
145 150 155

tta ctt gct ctc att ttc atc agc caa gtc aaa cgt cta aaa ccc aag 1371
Leu Leu Ala Leu Ile Phe Ile Ser Gln Val Lys Arg Leu Lys Pro Lys
160 165 170

cag cgc aga ctc ttt cat taagtcataa aaaatgggtgc gataaagcac 1419
Gln Arg Arg Leu Phe His
175

catttttcat ttctcgttcg gtatagatta aatttcttgc acgacaaact gcagggaatg 1479

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gctcatcttc tttaatcgta tcaggcattt gcgtaataag ccaatgtaaa tattctgaac 2019

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2060

&lt;210&gt; 12

&lt;211&gt; 178

&lt;212&gt; PRT

<213> *Pasteurella multocida*

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20 25 30Gln His Gly Met Gly Leu Ala Pro Cys Val Met Cys Ile Tyr Glu Arg  
35 40 45Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu Gly Leu Leu Tyr  
50 55 60Pro Ser Ser Met Leu Leu Arg Leu Val Ala Leu Leu Ile Gly Leu Ser  
65 70 75 80Ser Ala Ile Lys Gly Leu Met Ile Ser Ile Thr His Leu Asp Leu Gln  
85 90 95Leu Tyr Pro Ala Pro Trp Lys Gln Cys Ser Ala Val Ala Glu Phe Pro  
100 105 110Glu Thr Leu Pro Leu Asp Gln Trp Phe Pro Ala Leu Phe Leu Pro Ser  
115 120 125Gly Ser Cys Ser Glu Val Thr Trp Gln Phe Leu Gly Phe Ser Met Val  
130 135 140Gln Trp Ile Val Val Ile Phe Ala Leu Tyr Thr Leu Leu Ala Leu  
145 150 155 160Ile Phe Ile Ser Gln Val Lys Arg Leu Lys Pro Lys Gln Arg Arg Leu  
165 170 175

Phe His

&lt;210&gt; 13

&lt;211&gt; 4426

&lt;212&gt; DNA

<213> *Pasteurella multocida*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (2756)..(3211)

&lt;220&gt;

&lt;223&gt; exbB

&lt;400&gt; 13

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 Ile Arg Ser Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser  
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 Ser Glu Ser Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys  
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 Gly Thr Phe Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala  
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Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser Ser Asp Ser Thr Ser Thr
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 Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile  
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Val Lys Asp	Leu Thr Glu Val Leu Tyr Arg Ser Gly Tyr Val Thr Ser	
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cca acc cgt	ttt aga gat aaa aca atg tta tca gtc cta ccc aat tta	288
Pro Thr Arg	Phe Arg Asp Lys Thr Met Leu Ser Val Leu Pro Asn Leu	
	85 90 95	
atc gga aat	cgc tta agt att cac gac att gac cag ttg atc gaa atc	336
Ile Gly Asn	Arg Leu Ser Ile His Asp Ile Asp Gln Leu Ile Glu Ile	
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Glu Lys Gly	Ser Ser Asn Leu Asn Ile Glu Arg Gln Tyr Asp Val Phe	
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Gly Thr Asn	Asp Arg Trp Ser Phe Ser Ser Ser Tyr Arg Leu Tyr Lys	
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Asn His His	Ala Asn Gln Gln Arg Asn Tyr Thr Leu Ser Tyr Ser Gln	
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Pro Ile Gly	Phe Ser Thr Val Glu Ile Lys Ala Ser Glu Ser Thr Tyr	
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3247

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		195					200					205			
Pro	Ile	Gly	Phe	Ser	Thr	Val	Glu	Ile	Lys	Ala	Ser	Glu	Ser	Thr	Tyr
		210				215					220				
Glu	Lys	Glu	Leu	Arg	Gly	Ile	Asn	Thr	His	Ser	Ser	His	Gly	Lys	Thr
		225			230					235				240	
Gln	Ser	Leu	Ala	Val	Lys	Leu	Met	His	Val	Leu	Leu	Arg	Asn	Lys	Glu
			245						250					255	
Ser	Ile	Leu	Ser	Thr	Tyr	Thr	Glu	Phe	Glu	Phe	Lys	Lys	Arg	Ile	Ser
		260						265					270		
Tyr	Phe	Ser	Asp	Ile	Leu	Ile	Gly	Lys	Tyr	His	Asn	Asn	Lys	Val	Ser
		275					280					285			
Val	Gly	Leu	Ser	Tyr	Met	Thr	Asn	Phe	Ala	Tyr	Gly	Lys	Leu	Tyr	Ser
		290				295					300				
Asp	Ile	Ala	Tyr	Ala	Asn	Gly	Leu	Arg	Trp	Phe	Gly	Ala	Asn	Tyr	Ser
		305			310					315					320
Ala	Tyr	Asp	Ala	Asn	Arg	Glu	Lys	Thr	Leu	Lys	Leu	Leu	Ser	Gly	Ser
			325						330					335	
Ile	Asn	Trp	Gln	Arg	Pro	Ile	Ser	Leu	Phe	Glu	Arg	Ala	Met	Asn	Tyr
		340					345						350		

Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu  
 355 360 365  
 Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly  
 370 375 380  
 Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr  
 385 390 395 400  
 Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe  
 405 410 415  
 Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr  
 420 425 430  
 Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu  
 435 440 445  
 Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly  
 450 455 460  
 Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu  
 465 470 475 480  
 Ser Phe

<210> 21  
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 <212> DNA  
 <213> *Pasteurella multocida*

<220>  
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<220>  
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 gtacgataag atcgccatgc atttcattgt tttttatatt tccattgggt aatagactgg 180  
 tttcaaatg aaattggtca cttagtagca gtttgccggt taaggcgggt agcacttttt 240  
 gtgtactggc gggtaacata aaggtagctg cttgggtgcgc tacaattttt tcattacgat 300  
 ttaagttttt agccacaaaa cctaggtctg tcccttcggg taaatgagcg ttgatttcag 360  
 caagatcaat ctacgcataa ctgaaatgac tgacgagtaa actacatata agtatcggtc 420  
 gttgtaaaag gcgtaaaagc gtggcagtaa aaaaagaaga tattttatata ataattggct 480  
 cgagcaggtg ctattttttt attgtcgaa aataatagta ttgaaccct cgagagtaaa 540  
 tccttttttc gttaaacact tattttttta ttcaactacg gcattgtttt tacaatgttg 600

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tgggtttgtt tttatctaaa aaggaagaaa aaacgatt atg aaa cag att cca atg 656
Met Lys Gln Ile Pro Met
1 5

act ata cgt ggt gcg gaa caa tta aga caa gaa ctc gat ttt ttg aaa 704
Thr Ile Arg Gly Ala Glu Gln Leu Arg Gln Glu Leu Asp Phe Leu Lys
10 15 20

aac act cgt cgc cca gaa att att aat gct atc gca gaa gct cgt gaa 752
Asn Thr Arg Arg Pro Glu Ile Ile Asn Ala Ile Ala Glu Ala Arg Glu
25 30 35

cat ggc gat cta aaa gaa aat gca gaa tac cat gct gcg cgt gaa cag 800
His Gly Asp Leu Lys Glu Asn Ala Glu Tyr His Ala Ala Arg Glu Gln
40 45 50

caa gga ttt tgt gaa gga cga atc caa gaa att gaa ggg aaa tta gcg 848
Gln Gly Phe Cys Glu Gly Arg Ile Gln Glu Ile Glu Gly Lys Leu Ala
55 60 65 70

aat agt caa att att gat gtc aca aag atc cca aat aat ggc aaa gtg 896
Asn Ser Gln Ile Ile Asp Val Thr Lys Ile Pro Asn Asn Gly Lys Val
75 80 85

att ttt ggt gcc aca att ttg tta ctg aat att gac acg gaa gaa gaa 944
Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn Ile Asp Thr Glu Glu Glu
90 95 100

gtc tcg tac caa att gta ggc gat gat gaa gcc aat att aaa gca ggg 992
Val Ser Tyr Gln Ile Val Gly Asp Asp Glu Ala Asn Ile Lys Ala Gly
105 110 115

cta att tca gtt aac gcc acg cga ttg aat tagagaaagc taaatggatt 1042
Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
120 125

gcccaagatc ttggcgtaac aaaaacgtta attgacactt ccgtcatatac agcgattacg 1102

caaaatgcct taatggacga acaggcaaga attgagcaac atggcagatc accgaatact 1162

ttcgttga 1170

<210> 22
<211> 128
<212> PRT
<213> Pasteurella multocida

<400> 22
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20 25 30

Ile Ala Glu Ala Arg Glu His Gly Asp Leu Lys Glu Asn Ala Glu Tyr
35 40 45

His Ala Ala Arg Glu Gln Gln Gly Phe Cys Glu Gly Arg Ile Gln Glu
50 55 60

Ile Glu Gly Lys Leu Ala Asn Ser Gln Ile Ile Asp Val Thr Lys Ile
65 70 75 80

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Pro Asn Asn Gly Lys Val Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn
      85                      90                      95
Ile Asp Thr Glu Glu Val Ser Tyr Gln Ile Val Gly Asp Asp Glu
      100                      105
Ala Asn Ile Lys Ala Gly Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
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<210> 23
<211> 4666
<212> DNA
<213> Pasteurella multocida

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<220>
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<222> (980)..(2440)

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<220>
<223> guaB

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gcatcaatt tattcgatc aatcggttgt aatacttcaa tcagctctgc ccaaggttga 180
tcaatttgt gtgtttgttt tggaagaagc aaattaatgc caaagccaat cagcagatta 240
tgttgattat tctgacgatt ggcgatttcg accaaaaatc ctgctaattt gcgcccattg 300
aatagcacat catttgacca tttaaatcca atgttcaaag cacctgcttg cttagcggtt 360
tctgcgattg ccatacccac tactaaactc aagccttcta aattgacctt ttggtcacat 420
gccaataaca aactcataat cacttgacca gcaaaaggag aaagccattg acgaccacgt 480
cgtccacgtc cgcagtttg atattctgct aagcaaatag cgcctttttc caaatgtgca 540
atattgtcaa gcaagaattg attggtcgag ttaataatcg gcttaataata aagtggttaa 600
ggtgctaacg ctgctgcaa ataagattca tttaagcgac ttaattgagg tatgagacga 660
aaatgttgga ctgctgttc tatttgtatc ccttggttgt tcaatttttc gatatttgtt 720
aagatatctt gttctgaata acctaaaagt gcagtcgaatt ctgctaaaga aagttgttga 780
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aggcaactta ttatagacaa tgattttctc gaaaatcgat aaaaaaatcc attttcaaac 900
agcaacgaaa tctgtataat gcgaccgcaa tattttttac ctttttattt ttcataatca 960
cctaagagag aatattgca atg tta cga gta ata aaa gaa gca tta acc ttc 1012
Met Leu Arg Val Ile Lys Glu Ala Leu Thr Phe
      1                      5                      10
gat gat gtt ttg ctt gtc cca gca cat tct act gtg ctc cca aat acc 1060
Asp Asp Val Leu Leu Val Pro Ala His Ser Thr Val Leu Pro Asn Thr
      15                      20                      25

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gca gac ctt tcc act caa ctc acc aaa act atc cgc ctc aat atc cca	1108
Ala Asp Leu Ser Thr Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro	
30 35 40	
atg tta tcc gcc gcc atg gat acc gtg aca gaa act aaa ctg gca atc	1156
Met Leu Ser Ala Ala Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile	
45 50 55	
tct ctt gca caa gaa ggt ggc atc ggg ttt att cat aaa aat atg tct	1204
Ser Leu Ala Gln Glu Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser	
60 65 70 75	
att gag cgt caa gcg gaa cgt gtc cgc aaa gtg aaa aaa ttt gag agc	1252
Ile Glu Arg Gln Ala Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser	
80 85 90	
ggg att gta tcc gat cct gtc acc gtt tca cca acc tta tct tta gca	1300
Gly Ile Val Ser Asp Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala	
95 100 105	
gaa tta agt gaa tta gtg aag aaa aat ggt ttt gcg agt ttc cct gtt	1348
Glu Leu Ser Glu Leu Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val	
110 115 120	
ggt gat gat gaa aaa aat ctt gtc ggt atc att act ggt cgt gat aca	1396
Val Asp Asp Glu Lys Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr	
125 130 135	
cgc ttt gtc acg gat tta aat aaa aca gtg gcg gac ttt atg acc cct	1444
Arg Phe Val Thr Asp Leu Asn Lys Thr Val Ala Ala Asp Phe Met Thr Pro	
140 145 150 155	
aaa gct cgt ctt gtc acg gtg aaa cgc aat gca agt cgc gat gaa att	1492
Lys Ala Arg Leu Val Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile	
160 165 170	
ttt ggt cta atg cat aca cac cgt gta gaa aaa gtc ctt gtt gtc agc	1540
Phe Gly Leu Met His Thr His Arg Val Glu Lys Val Leu Val Val Ser	
175 180 185	
gac gat ttc aaa tta aaa ggc atg atc acc tta aaa gac tac caa aaa	1588
Asp Asp Phe Lys Leu Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys	
190 195 200	
tcc gag caa aaa cca caa gcc tgt aaa gat gaa ttt ggt cgt tta cgt	1636
Ser Glu Gln Lys Pro Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg	
205 210 215	
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Val Gly Ala Ala Val Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp	
220 225 230 235	
gca tta gtg aaa gca ggg gtc gat gtg tta ttg att gac tca tca cac	1732
Ala Leu Val Lys Ala Gly Val Asp Val Leu Leu Ile Asp Ser Ser His	
240 245 250	
ggg cat tca gaa ggt gtg tta caa cgt gtg cgt gaa act cgt gcg aaa	1780
Gly His Ser Glu Gly Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys	
255 260 265	
tac cca gat ttg cca att gtt gca ggt aat gtg gca acc gct gaa ggc	1828
Tyr Pro Asp Leu Pro Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly	
270 275 280	

gca att gcg ttg gct gat gca ggg gca agt gca gtg aaa gtg ggg att 1876  
 Ala Ile Ala Leu Ala Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile  
 285 290 295

ggc cct ggt tca att tgc aca aca cgt att gtc aca gcc gtg ggc gtt 1924  
 Gly Pro Gly Ser Ile Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val  
 300 305 310 315

cca caa att aca gcg att gcc gat gcg gca gaa gca cta aaa gat cgg 1972  
 Pro Gln Ile Thr Ala Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg  
 320 325 330

ggc att cct gtg att gca gat ggc ggt atc cgt ttc tct ggt gat att 2020  
 Gly Ile Pro Val Ile Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile  
 335 340 345

tcg aaa gcc att gcg gcg ggc gcc tct tgt gtt atg gtg ggt tcc atg 2068  
 Ser Lys Ala Ile Ala Ala Gly Ala Ser Cys Val Met Val Gly Ser Met  
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ttt gca ggt aca gaa gaa gca cca ggt gaa atc gaa ctt tat caa ggt 2116  
 Phe Ala Gly Thr Glu Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly  
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cgt gcc ttt aaa tct tat cga ggt atg gga tcg tta ggt gcg atg agc 2164  
 Arg Ala Phe Lys Ser Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser  
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aaa ggc tca agc gac gcg tat ttc cag tcc gat aat gca gct gac aaa 2212  
 Lys Gly Ser Ser Asp Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys  
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tta gta cca gaa ggt att gaa gga cgt att cca tat aaa gga ttc tta 2260  
 Leu Val Pro Glu Gly Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu  
 415 420 425

aaa gaa att atc cat caa caa atg ggt gga ttg cgt tct tgt atg ggc 2308  
 Lys Glu Ile Ile His Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly  
 430 435 440

tta acg ggt tgt gca acc att gat gaa ctc cgt acc aaa gcg cag ttt 2356  
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 445 450 455

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 Thr Ile Thr Lys Glu Ala Pro Asn Tyr Arg Met Gly  
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<210> 24  
 <211> 487  
 <212> PRT  
 <213> *Pasteurella multocida*

<400> 24

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Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr
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Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala
          35             40             45

Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu
          50             55             60

Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala
          65             70             75             80

Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Asp
          85             90             95

Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala Glu Leu Ser Glu Leu
          100            105            110

Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val Val Asp Asp Glu Lys
          115            120            125

Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp
          130            135            140

Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro Lys Ala Arg Leu Val
          145            150            155            160

Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile Phe Gly Leu Met His
          165            170            175

Thr His Arg Val Glu Lys Val Leu Val Val Ser Asp Asp Phe Lys Leu
          180            185            190

Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ser Glu Gln Lys Pro
          195            200            205

Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val
          210            215            220

Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala
          225            230            235            240

Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly
          245            250            255

Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro
          260            265            270

Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala
          275            280            285

Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile
          290            295            300

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Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala  
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 Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg Gly Ile Pro Val Ile  
 325 330 335  
 Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile Ser Lys Ala Ile Ala  
 340 345 350  
 Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu  
 355 360 365  
 Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser  
 370 375 380  
 Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp  
 385 390 395 400  
 Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly  
 405 410 415  
 Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu Lys Glu Ile Ile His  
 420 425 430  
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 435 440 445  
 Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe Val Arg Ile Ser Gly  
 450 455 460  
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<210> 25  
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 <212> DNA  
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 <222> (191)..(1828)

<220>  
 <223> H11501

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 aattgacggc gatttagggc gtgatgaatt tgatgacggc gatttatata gtatttggcg 180  
 gagataaaaa atg gcg aag aaa aag aaa aaa tta caa caa gcg aaa aaa 229  
 Met Ala Lys Lys Lys Lys Lys Leu Gln Gln Ala Lys Lys  
 1 5 10  
 gta caa gtt ggc tta gat aca caa aca aat gag gcg cgt gtc acg gag 277  
 Val Gln Val Gly Leu Asp Thr Gln Thr Asn Glu Ala Arg Val Thr Glu  
 15 20 25

aca gga aga att att tct gat cac cca agc aat aaa att acc ccc gca Thr Gly Arg Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala 30 35 40 45	325
aag tta aaa ggg att tta gaa gat gct gaa ggt ggt gat att acc gcg Lys Leu Lys Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala 50 55 60	373
caa cat gag ctt ttc atg gat att gaa gaa cgc gac agt tgc atc ggg Gln His Glu Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly 65 70 75	421
gca aat att caa acc cgt aag cgt gcg att tta acc ctt gac tgg cgc Ala Asn Ile Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg 80 85 90	469
att gca gag cca cgt aat gcc aca ccg caa gaa gaa aaa ctg caa gtc Ile Ala Glu Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val 95 100 105	517
gaa att gac gag ctt ttc tat caa ttc cca atg cta gaa gat tta atg Glu Ile Asp Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met 110 115 120 125	565
gtg gat atg atg gat gcg gta gga cat ggt ttt tcg gcg tta gaa att Val Asp Met Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile 130 135 140	613
gaa tgg aag caa gct gaa agt aaa tgg att cca gtt aat ttt atc gca Glu Trp Lys Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala 145 150 155	661
cgt ccg cag tcg tgg ttt aaa cta gac aag gat gat aat tta ctg ctt Arg Pro Gln Ser Trp Phe Lys Leu Asp Lys Asp Asn Leu Leu Leu 160 165 170	709
aaa acg cca gat aat caa gac ggt gag ccg ttg aga caa tat ggc tgg Lys Thr Pro Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp 175 180 185	757
gta gtg cat acc cac aaa tca aga aca gta cag ctt gct cgt atg ggt Val Val His Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly 190 195 200 205	805
tta ttt aga acg ctc gca tgg ctt tat atg ttt aaa cac tac tcg gtg Leu Phe Arg Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val 210 215 220	853
cat gat ttt gcc gaa ttt cta gag ctt tat ggt atg ccg att cgt att His Asp Phe Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile 225 230 235	901
ggt aaa tac cca ttt ggg gca acg aat gac gaa aag cgc aca tta ttg Gly Lys Tyr Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu 240 245 250	949
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370 375 380	
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415 420 425	
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430 435 440 445	
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465 470 475	
ctt gcg caa gca ttt aat gag cct gat ttt aat aaa caa tta aat cca Leu Ala Gln Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro	1669
480 485 490	
atg gta aag aaa gct gtt gcg gta ctc atg gca tgt gac tct tac gat Met Val Lys Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp	1717
495 500 505	
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510 515 520 525	
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 Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg Ile Ala Glu  
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 Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val Glu Ile Asp  
 100 105 110  
 Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met Val Asp Met  
 115 120 125  
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 Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala Arg Pro Gln  
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 Ser Trp Phe Lys Leu Asp Lys Asp Asp Asn Leu Leu Leu Lys Thr Pro  
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Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp Val Val His  
 180 185 190  
 Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly Leu Phe Arg  
 195 200 205  
 Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val His Asp Phe  
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 225 230 235 240  
 Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu Arg Ala Leu  
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 Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu Gly Met Asn  
 260 265 270  
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 275 280 285  
 Pro Phe Leu Gln Met Val Asp Trp Cys Glu Lys Ser Ala Ala Arg Leu  
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 405 410 415  
 Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp Leu Asn Asp  
 420 425 430  
 Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln Asn His Val  
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 Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro Met Val Lys  
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 Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp Glu Ala Ala  
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Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His Glu His Glu  
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Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu  
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Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu  
35 40 45  
cgt tat ggt att gaa tat cga tat aac ggc ttg tct tgg ttg gaa acg 193  
Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr  
50 55 60  
gta aag ctt ttt ttg gca aag cag aaa atc gaa caa cgt tct gct ctc 241  
Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu  
65 70 75 80

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Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys	85 90 95
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Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr	100 105 110
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Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe	115 120 125
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Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe	130 135 140
cgg cgg tgg caa atc aat ana ttc aga caa caa ggt cga aat aac tat	481
Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr	145 150 155 160
aca gaa gtg ttt ccc gtt aaa tcc cga gag ttt tct ttt tct ctt atg	529
Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met	165 170 175
gac gac att aag att ggc gaa ttg cta cat ctc gga ttg ggc ggt cgg	577
Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Arg	180 185 190
tgg gat cac tat aac tat aag cca tta tta aat tct cag cat aat atc	625
Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Ser His Asn Ile	195 200 205
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Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr	245 250 255
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Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp	260 265 270
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Leu Gln Pro Glu Thr Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln	275 280 285
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Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His	290 295 300
aac ttt att caa gaa cgt gag atg acc tgt gat aaa att cca tat gag	961
Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu	305 310 315 320
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Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His	325 330 335

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 Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu  
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 Val Asn Glu Pro Glu Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala  
 340 345 350

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                   405                                  410                                  415  
 Lys Asp Ala Ile Glu Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys  
                   420                                  425                                  430  
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Cys Gly Ile Gln Ile Gly Leu Ala Ser Asn Pro Asn Pro Pro Asp Val
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gat gag tta tta cct att att gtg aat gct gat gaa gat aat aaa tta 1221
Asp Glu Leu Leu Pro Ile Ile Val Asn Ala Asp Glu Asp Asn Lys Leu
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Pro Gly Arg Ser Val Leu Lys Gln Lys Asn Ile Asp Gln Gln Gln Ala
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cta cta ttt ggt tta cag tgg tta aaa aat aaa aga aat acc ctt atg Leu Leu Phe Gly Leu Gln Trp Leu Lys Asn Lys Arg Asn Thr Leu Met 370 375 380	2229
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 tyr lys thr ala lys glu gly gly leu pro asn tyr leu ile leu 470  
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cct aat tct aaa ggt tat ctt cct tat gat tat aaa gaa agg gat ctt 6231  
 pro asn ser lys gly tyr leu pro tyr asp tyr lys glu arg asp leu 490  
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cca gtt gaa gca acg aca cag tca tta tat ttt gca aat att ctt aag Pro Val Glu Thr Thr Gln Ser Leu Tyr Phe Ala Asn Ile Leu Lys 575 580 585	6519
gta cat aat atg att agc ata gat tta gga tat cgt tat gat cat att Val His Asn Met Ile Ser Ile Asp Leu Gly Tyr Arg Tyr Asp His Ile 590 595 600	6567
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Thr Ser Val Phe Gln Thr Lys Tyr Arg His Phe Ile Asp Leu Ala Tyr	
750 755 760	
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Arg Asp Phe Gln Val Tyr Gln Asn Val Asn Val Asp Asn Ala Lys Val	
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Lys Gly Leu Leu Ile Asn Ala Arg Leu Asn Lys Gly Tyr Phe Thr His	
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Val Leu Asp Gly Phe Asn Thr Ser Tyr Lys Phe Thr Tyr Gln Arg Gly	
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Leu Tyr Ile Thr Arg Val Ser Glu Lys Lys Ala Lys Asp Thr Tyr Asn	
860 865 870	
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Ser Asp Asp Tyr Thr Leu Val Asp Ala Val Gly Tyr Ile Lys Pro Ile	
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 Glu Lys Lys Ile Gly Glu Thr Val Lys Thr Ala Ser Gln Leu Lys Arg  
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 Thr Val Val Glu Ala Gly Arg Phe Gly Ser Ser Gly Tyr Ala Ile Arg  
           85          90          95  
 Gly Val Asp Glu Asn Arg Val Ala Ile Thr Val Asp Gly Leu His Gln  
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 Ala Glu Thr Leu Ser Ser Gln Gly Phe Lys Glu Leu Phe Glu Gly Tyr  
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 Gly Asn Phe Asn Asn Thr Arg Asn Ser Val Glu Ile Glu Thr Leu Lys  
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 Val Ala Lys Ile Ala Lys Gly Ala Asp Ser Val Lys Val Gly Ser Gly  
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 Ser Leu Gly Gly Ala Val Leu Phe Glu Thr Lys Asp Ala Arg Asp Phe  
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 Leu Thr Glu Lys Asp Trp His Ile Gly Tyr Lys Ala Gly Tyr Ser Thr  
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 Ala Asp Asn Gln Gly Leu Asn Ala Val Thr Leu Ala Gly Arg Tyr Gln  
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 Glu Lys Ala Asp Pro Tyr Thr Ile Thr Lys Glu Ser Thr Leu Val Lys  
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 Phe Ser Phe Ser Pro Thr Glu Asn His Arg Phe Thr Val Ala Ser Asp  
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 Thr Tyr Leu Gln His Ser Arg Gly His Asp Leu Ser Tyr Asn Leu Val  
   275          280          285  
 Ala Thr Thr His Ile Gln Leu Asp Glu Lys Glu Ser Arg His Ala Asn  
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Asp Leu Thr Lys Arg Lys Asn Val Ser Phe Thr Tyr Glu Asn Tyr Thr  
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 Cys Asp Ser Tyr Lys Asn Pro Leu Gly Leu Gln Phe Lys Asp Gly Gln  
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 450 455 460  
 Glu Gly Gly Leu Pro Asn Tyr Leu Ile Leu Pro Asn Ser Lys Gly Tyr  
 465 470 475 480  
 Leu Pro Tyr Asp Tyr Lys Glu Arg Asp Leu Asn Thr Asn Thr Lys Gln  
 485 490 495  
 Ile Asn Leu Asp Leu Thr Lys Thr Phe Leu Thr Phe Asn Ile Glu Asn  
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 545 550 555 560  
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 565 570 575  
 Gln Ser Leu Tyr Phe Ala Asn Ile Leu Lys Val His Asn Met Ile Ser  
 580 585 590  
 Ile Asp Leu Gly Tyr Arg Tyr Asp His Ile Lys Tyr Asn Pro Glu Tyr  
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 625 630 635 640

Tyr Ala Lys Phe Gly Glu Ala Tyr Lys Lys Trp Lys Glu Tyr Leu Pro  
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 Lys Asn Ala Glu Glu Asn Ile Ala Tyr Ile Ala Gln Asp Lys Thr Phe  
 660 665 670  
 Lys Lys His Ser Tyr Ser Leu Gly Ala Thr Phe Asp Pro Leu Asn Phe  
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 Thr Val His Asp Asn Trp Gly Phe Val Ser Thr Ser Val Phe Gln Thr  
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 Lys Tyr Arg His Phe Ile Asp Leu Ala Tyr Leu Gly Ser Arg Asn Leu  
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 Ser Asn Ser Val Gly Gly Gln Ala Gln Ala Arg Asp Phe Gln Val Tyr  
 770 775 780  
 Gln Asn Val Asn Val Asp Asn Ala Lys Val Lys Gly Leu Glu Ile Asn  
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 Ala Arg Leu Asn Leu Gly Tyr Phe Trp His Val Leu Asp Gly Phe Asn  
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 Pro Met Asn Ala Ile Gln Pro Lys Ala Ser Val Phe Gly Leu Gly Tyr  
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 Ser Glu Lys Lys Ala Lys Asp Thr Tyr Asn Met Phe Tyr Lys Glu Gln  
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 Gly Tyr Lys Asp Ser Ala Val Arg Trp Arg Ser Asp Asp Tyr Thr Leu  
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 Val Asp Ala Val Gly Tyr Ile Lys Pro Ile Lys Asn Leu Thr Leu Gln  
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 Phe Gly Val Tyr Asn Leu Thr Asp Arg Lys Tyr Leu Thr Trp Glu Ser  
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 Ala Arg Ser Ile Lys Pro Phe Gly Thr Ser Asn Leu Ile Asn Gln Lys  
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Tyr Phe Leu Trp Phe Ile Leu Phe Ile Leu Ser Ile Tyr Leu Phe Ile
10 15 20 25

acc ata caa gaa aga cga ggt tat tgt ttt gac aaa cgt gca tat att 1228
Thr Ile Gln Glu Arg Arg Gly Tyr Cys Phe Asp Lys Arg Ala Tyr Ile
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 Tyr Cys Phe Asp Lys Arg Ala Tyr Ile His Glu Leu Tyr Thr Glu Gln  
 35 40 45  
 Glu Leu Ile Asp Arg Gly Ile Glu Tyr Val Val Ser Thr Met Pro Ser  
 50 55 60  
 Gly Val Ile Lys Pro Asp Gly Thr Ile Lys Glu Val Lys Arg Tyr Thr  
 65 70 75 80  
 Ser Val Glu Glu Phe Lys Gln Met Asn Pro Ala Cys Cys Thr Leu Thr  
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 Thr Phe Ile Asp Glu Gly Gly Asp Gly Tyr Pro Asp Asp Asp Gly Tyr  
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 Gly Tyr Val Arg Ile Glu Tyr Leu Arg His Tyr Val Glu Asn Leu Lys  
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gcagaactgg ctatcttctc acttttagat aattgtatta ttaaaagaag ctgtatgatt 180
gttattctat cattagtggg taataaatat tctttatttt ttgagagata aaaacaattc 240
atatttcaat agaaaacaga aaataaagat tatcaaaaga attatccgtc cttataaata 300
tgagtctgta ttgtgagatg atat atg aat att tta ttt gtt tct gat gat 351
                               Met Asn Ile Leu Phe Val Ser Asp Asp
                               1           5

ggt tat gct aaa cat ctg gtg gtt gcg att aaa agc att ata aat cat 399
Val Tyr Ala Lys His Leu Val Val Ala Ile Lys Ser Ile Ile Asn His
10           15           20           25

aat gaa aaa ggt att tca ttt tat att ttt gat ttg ggt ata aag gat 447
Asn Glu Lys Gly Ile Ser Phe Tyr Ile Phe Asp Leu Gly Ile Lys Asp
30           35           40

gaa aat aag aga aat att aat gat att gtt tct tct tat gga agt gaa 495
Glu Asn Lys Arg Asn Ile Asn Asp Ile Val Ser Ser Tyr Gly Ser Glu
45           50           55

gtc aac ttt att gct gtg aat gag aaa gaa ttt gag agt ttt cct gtt 543
Val Asn Phe Ile Ala Val Asn Glu Lys Glu Phe Glu Ser Phe Pro Val
60           65           70

caa att agt tat att tct tta gca aca tat gca agg cta aaa gcg gca 591
Gln Ile Ser Tyr Ile Ser Leu Ala Thr Tyr Ala Arg Leu Lys Ala Ala
75           80           85

gag tat ttg ccg gat aat tta aat aaa att att tat tta gat gtt gat 639
Glu Tyr Leu Pro Asp Asn Leu Asn Lys Ile Ile Tyr Leu Asp Val Asp
90           95           100           105

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gtt ttg gtt ttt aac tca tta gaa atg tta tgg aat gtt gat gtt aat 687  
 Val Leu Val Phe Asn Ser Leu Glu Met Leu Trp Asn Val Asp Val Asn  
 110 115 120

aat ttt ctt acc gca gcc tgt tat gat tct ttc atc gaa aat gaa aag 735  
 Asn Phe Leu Thr Ala Ala Cys Tyr Asp Ser Phe Ile Glu Asn Glu Lys  
 125 130 135

tct gag cat aaa aaa tcg att tca atg tca gat aag gaa tat tat ttt 783  
 Ser Glu His Lys Lys Ser Ile Ser Met Ser Asp Lys Glu Tyr Trp Phe  
 140 145 150

aat gca gga gta atg cta ttt aat tta gat gaa tgg cgg aag atg gat 831  
 Asn Ala Gly Val Met Leu Phe Asn Leu Asp Glu Trp Arg Lys Met Asp  
 155 160 165

gta ttc tca aga gct tta gac ctg tta gct atg tat cct aat caa atg 879  
 Val Phe Ser Arg Ala Leu Asp Leu Leu Ala Met Tyr Pro Asn Glu Met  
 170 175 180 185

att tat cag gat caa gat ata ttg aat atc ctt ttt agg aat aaa gtc 927  
 Ile Tyr Gln Asp Gln Asp Ile Leu Asn Ile Leu Phe Arg Asn Lys Val  
 190 195 200

tgt tat tta gat tgc aga ttt aat ttc atg cca aat caa ctt gaa aga 975  
 Cys Tyr Leu Asp Cys Arg Phe Asn Phe Met Pro Asn Gln Leu Glu Arg  
 205 210 215

ata aan caa tac cat aaa gga aaa ntg agc aac tta cat tct tta gaa 1023  
 Ile Xaa Gln Tyr His Lys Gly Lys Xaa Ser Asn Leu His Ser Leu Glu  
 220 225 230

aaa aca acg atg cct gtc gtt att tca cat tat tgt ggt cca gaa aaa 1071  
 Lys Thr Thr Met Pro Val Val Ile Ser His Tyr Cys Gly Pro Glu Lys  
 235 240 245

gcg tgg cat gcg gat tgt aaa cat ttt aat gta tat ttc tat cag aaa 1119  
 Ala Trp His Ala Asp Cys Lys His Phe Asn Val Tyr Phe Tyr Gln Lys  
 250 255 260 265

ata tta gca naa atn tcg aga ggc ncg gat aaa gaa cgc gta tta tct 1167  
 Ile Leu Ala Xaa Xaa Ser Arg Gly Xaa Asp Lys Glu Arg Val Leu Ser  
 270 275 280

ata aaa act tat ctc aag gcc ttg att aga agg att aga tat aaa ttc 1215  
 Ile Lys Thr Tyr Leu Lys Ala Leu Ile Arg Arg Ile Arg Tyr Lys Phe  
 285 290 295

aaa tat caa gtc tat taactattga atttttgc aa atgagataag agtatagtgc 1270  
 Lys Tyr Gln Val Tyr  
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ttattttcta aaagaaaaa atcttcttgt agattgagtg attctatttg ttctctaat 1630

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                   20                  25                  30  
 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn  
           35                  40                  45  
 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn  
           50                  55                  60  
 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu  
           65                  70                  75                  80  
 Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu  
                   85                  90                  95  
 Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu  
                   100                  105                  110  
 Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys  
           115                  120                  125  
 Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile  
           130                  135                  140

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Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
145                      150                      155                      160

Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp
                      165                      170                      175

Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile
                      180                      185                      190

Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
                      195                      200                      205

Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Xaa Gln Tyr His Lys Gly
210                      215                      220

Lys Xaa Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
225                      230                      235                      240

Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
                      245                      250                      255

His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Xaa Xaa Ser Arg
                      260                      265                      270

Gly Xaa Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala
275                      280                      285

Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr
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<212> DNA
<213> Pasteurella multocida

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gga cac cca gat gca gaa gct cgt aca aaa ttc gtc att aaa gaa tta 97
Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
      20             25             30

nat aat aaa ggc att caa gat gag caa tta ttc atc gac acg ggg atg 145
Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
      35             40             45

tgg gat gcc gct tta gcg aaa gat aaa atg gat gca tgg tta tct agc 193
Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
      50             55             60

tct aaa gca aat caa att gaa gtg atc atc gct aac aac gat ggt atg 241
Ser Lys Ala Asn Gln Ile Glu Val Ile Ala Asn Asn Asp Gly Met
      65             70             75             80

gcg atg ggg gca ttg gaa gcc acg aaa gca cat ggt aaa aaa tta cca 289
Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
      85             90             95

atc ttc ngt gta nat gcg tta cca gaa gtc ctc caa tta atc aaa aaa 337
Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
      100            105            110

ggg gaa att gca ggt acg gtg tta aat gac ggt gtg aac caa ggt aaa 385
Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
      115            120            125

gcc gtt gtt caa tta agt aat aat ctt gca aaa gga aaa cct gcc act 433
Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
      130            135            140

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Cys Trp Cys Gly Cys Gly
165

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gtatcgacat tgggtcgaaa tatgaaattt atcagctgat tatggagtta gcaaaaaaag 1969
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<210> 38
<211> 166
<212> PRT
<213> Pasteurella multocida

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Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
          20           25           30

Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
          35           40           45

Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
          50           55           60

Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
          65           70           75           80

Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
          85           90           95

Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
          100          105          110

Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
          115          120          125

Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
          130          135          140

Glu Gly Thr Lys Trp Gln Leu Lys Arg Ser Cys Pro Thr Tyr Pro Leu
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Cys Trp Cys Gly Cys Gly
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<212> DNA
<213> Pasteurella multocida

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ctcattatta ggcaaaattg ataacgtata attcacttct tattaaggct tagtttttct 300
aagccttatt ttttaggaga aatta atg aaa aca aaa att tgt att atc act 352
Met Lys Thr Lys Ile Cys Ile Ile Thr
1 5
ggc agt acg ctt ggt ggt gca gaa tat gtt gca gaa cat att gct gaa 400
Gly Ser Thr Leu Gly Gly Ala Glu Tyr Val Ala Glu His Ile Ala Glu
10 15 20 25
ata tta gaa caa caa gat tat cct gta cgt tta gaa cat gga cca aat 448
Ile Leu Glu Gln Gln Asp Tyr Pro Val Arg Leu Glu His Gly Pro Asn
30 35 40
ttt gaa gaa gtg atc gat gaa aaa tgt tgg ctt gtt gtc acc tct acc 496
Phe Glu Glu Val Ile Asp Glu Lys Cys Trp Leu Val Val Thr Ser Thr
45 50 55
cat ggt gca ggt gaa tta ccg gat aat att aaa cct ctg ttt gaa aaa 544
His Gly Ala Gly Glu Leu Pro Asp Asn Ile Lys Pro Leu Phe Glu Lys
60 65 70
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Leu Ala Phe His Pro Lys Gln Leu Ala Asp Leu Arg Phe Ala Val Ile
75 80 85
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Gly Leu Gly Asn Ser Asp Tyr Asp Thr Phe Cys His Ala Val Asp His
90 95 100 105
gtg gaa caa tta ctg cta agc aaa gat gct tta caa ctg tgt gaa tcg 688
Val Glu Gln Leu Leu Ser Lys Asp Ala Leu Gln Leu Cys Glu Ser
110 115 120
cta aga atg gat atg cta acc att act gat cct gaa cac acg gcc gaa 736
Leu Arg Met Asp Met Leu Thr Ile Thr Asp Pro Glu His Thr Ala Glu
125 130 135
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Gln Trp Leu Pro Gln Phe Leu Ser Gln Leu
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&lt;210&gt; 40

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 40

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Glu Tyr Val Ala Glu His Ile Ala Glu Ile Leu Glu Gln Gln Asp Tyr
 20             25             30

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Pro Val Arg Leu Glu His Gly Pro Asn Phe Glu Glu Val Ile Asp Glu
 35             40             45

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aaaccaattg ccgtcatttt ccacgcctct taagcgacgg cgcattggctt cttgttgttc 2760

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aatttagttc agcgggaattc tt atg tta ttt aaa aaa att cga ggc tta ttt 3232
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Ser Asn Asp Leu Ser Ile Asp Leu Gly Thr Ala Asn Thr Leu Ile Tyr
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gtc aaa gga caa ggg att gtt tta gat gaa cct tct gtt gtg gcg att 3328
Val Lys Gly Gln Gly Ile Val Leu Asp Glu Pro Ser Val Val Ala Ile
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cgc caa gaa cgt tca ggt gca tta aaa agc att gct gcg gtt ggt cgt 3376
Arg Gln Glu Arg Ser Gly Ala Leu Lys Ser Ile Ala Ala Val Gly Arg
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gat gcc aaa tta atg tta ggc cgt aca ccg aaa agc att gca gcg att 3424
Asp Ala Lys Leu Met Leu Gly Arg Thr Pro Lys Ser Ile Ala Ala Ile
                        60 65 70
cgt cct atg aaa gat ggg gtg atc gca gat ttc ttt gtg aca gaa aaa 3472
Arg Pro Met Lys Asp Gly Val Ile Ala Asp Phe Phe Val Thr Glu Lys
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Met Leu Gln Tyr Phe Ile Lys Gln Val His Ser Ser Asn Phe Met Arg
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Glu Arg Arg Ala Ile Lys Glu Ser Ala Ile Gly Ala Gly Ala Arg Glu
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Val Tyr Leu Ile Glu Glu Pro Met Ala Ala Ala Ile Gly Ala Lys Leu
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cct gtt tcg act gcc aca ggt tcg atg gtg atc gat atc ggt ggt ggt 3712
Pro Val Ser Thr Ala Thr Gly Ser Met Val Ile Asp Ile Gly Gly Gly
                        155 160 165 170
acg acg gaa gtt gcg gtg att tct tta aat ggc att gtg tat tcc tct 3760
Thr Thr Glu Val Ala Val Ile Ser Leu Asn Gly Ile Val Tyr Ser Ser
                        175 180 185
tca gtc cgc att ggt ggt gat cgt ttt gat gag gcg att att tct tat 3808

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Ser Val Arg Ile Gly Gly Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr
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gta cgc aag acg ttc ggt tca att att ggg gaa ccg aca gca gag cgt 3856
Val Arg Lys Thr Phe Gly Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg
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atc aaa caa gag att ggt agt gcg ttt att caa gaa ggc gat gaa gtc 3904
Ile Lys Gln Glu Ile Gly Ser Ala Phe Ile Gln Glu Gly Asp Glu Val
      220      225      230
cgt gaa att gaa gtg cat ggt cat aac tta gca gaa ggt gcg ccg cgt 3952
Arg Glu Ile Glu Val His Gly His Asn Leu Ala Glu Gly Ala Pro Arg
      235      240      245      250
tct ttc aaa ctc acc tca cgt gat gtg tta gaa gct att caa gcc ccg 4000
Ser Phe Lys Leu Thr Ser Arg Asp Val Leu Glu Ala Ile Gln Ala Pro
      255      260      265
tta aat ggc att gtt gcg gca gtg cgc acg gcc ttg gaa gag tgt caa 4048
Leu Asn Gly Ile Val Ala Ala Val Arg Thr Ala Leu Glu Glu Cys Gln
      270      275      280
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Pro Glu His Ala Ala Asp Ile Phe Glu Arg Gly Met Val Leu Thr Gly
      285      290      295
ggc ggt gcc ctt att cgt aat att gat gtt tta ctg tca aaa gaa acc 4144
Gly Gly Ala Leu Ile Arg Asn Ile Asp Val Leu Leu Ser Lys Glu Thr
      300      305      310
ggg gtg ccg gtt atc atc gcc gat gat cct tta acc tgt gtt gcc cgt 4192
Gly Val Pro Val Ile Ile Ala Asp Asp Pro Leu Thr Cys Val Ala Arg
      315      320      325      330
ggg ggt ggc gag gca tta gag atg atc gat atg cac ggt ggt gat att 4240
Gly Gly Gly Glu Ala Leu Glu Met Ile Asp Met His Gly Gly Asp Ile
      335      340      345
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Phe Ser Asp Asp Ile
      350
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&lt;210&gt; 42

&lt;211&gt; 351

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 42

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 20 25 30

Val Leu Asp Glu Pro Ser Val Val Ala Ile Arg Gln Glu Arg Ser Gly  
 35 40 45

Ala Leu Lys Ser Ile Ala Ala Val Gly Arg Asp Ala Lys Leu Met Leu  
 50 55 60

Gly Arg Thr Pro Lys Ser Ile Ala Ala Ile Arg Pro Met Lys Asp Gly  
 65 70 75 80

Val Ile Ala Asp Phe Phe Val Thr Glu Lys Met Leu Gln Tyr Phe Ile  
 85 90 95

Lys Gln Val His Ser Ser Asn Phe Met Arg Pro Ser Pro Arg Val Leu  
 100 105 110

Val Cys Val Pro Ala Gly Ala Thr Gln Val Glu Arg Arg Ala Ile Lys  
 115 120 125

Glu Ser Ala Ile Gly Ala Gly Ala Arg Glu Val Tyr Leu Ile Glu Glu  
 130 135 140

Pro Met Ala Ala Ala Ile Gly Ala Lys Leu Pro Val Ser Thr Ala Thr  
 145 150 155 160

Gly Ser Met Val Ile Asp Ile Gly Gly Gly Thr Thr Glu Val Ala Val  
 165 170 175

Ile Ser Leu Asn Gly Ile Val Tyr Ser Ser Ser Val Arg Ile Gly Gly  
 180 185 190

Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr Val Arg Lys Thr Phe Gly  
 195 200 205

Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg Ile Lys Gln Glu Ile Gly  
 210 215 220

Ser Ala Phe Ile Gln Glu Gly Asp Glu Val Arg Glu Ile Glu Val His  
 225 230 235 240

Gly His Asn Leu Ala Glu Gly Ala Pro Arg Ser Phe Lys Leu Thr Ser

245	250	255	
Arg Asp Val Leu Glu Ala Ile Gln Ala	Pro Leu Asn Gly Ile Val Ala		
260	265	270	
Ala Val Arg Thr Ala Leu Glu Glu Cys Gln Pro Glu His Ala Ala Asp			
275	280	285	
Ile Phe Glu Arg Gly Met Val Leu Thr Gly Gly Gly Ala Leu Ile Arg			
290	295	300	
Asn Ile Asp Val Leu Leu Ser Lys Glu Thr Gly Val Pro Val Ile Ile			
305	310	315	320
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gaa aaa gtg aaa gcg att gca gaa gcg cgt tta ggc gaa gca tac cgt			96
Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly Glu Ala Tyr Arg			
20	25	30	
atc act gaa aac aag cac gtt atg aac aaa att gat gcg att aaa gct			144
Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala			
35	40	45	
gat gtg att gca caa atc aca gct gaa gta gca gaa ggc gaa gac atc			192
Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile			
50	55	60	
agt gaa ggg aaa att gtc gat att ttc acc gca ctt gaa agc caa atc			240
Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile			
65	70	75	80
gta cgt agc cgt atc att gct ggt gaa cca cgt att gat ggt cgt aca			288
Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr			
85	90	95	
gtg gat act gtt cgt gca tta gat att tgt act ggt gtt tta cca cgt			336
Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg			
100	105	110	
aca cac ggt tct gcg att ttc acc cgt ggt gaa aca cag gcg tta gct			384

Thr	His	Gly	Ser	Ala	Ile	Phe	Thr	Arg	Gly	Glu	Thr	Gln	Ala	Leu	Ala		
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Val	Ala	Thr	Leu	Gly	Thr	Glu	Arg	Asp	Ala	Gln	Ile	Ile	Asp	Glu	Leu		
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aca	ggc	gag	cgt	tca	gat	cac	ttc	tta	ttc	cac	tac	aac	ttc	ccg	cca	480	
Thr	Gly	Glu	Arg	Ser	Asp	His	Phe	Leu	Phe	His	Tyr	Asn	Phe	Pro	Pro		
	145				150				155					160			
tat	tct	gtg	ggc	gaa	acc	ggc	atg	att	ggc	tca	cca	aaa	cgt	cgt	gaa	528	
Tyr	Ser	Val	Gly	Glu	Thr	Gly	Met	Ile	Gly	Ser	Pro	Lys	Arg	Arg	Glu		
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att	ggc	cat	ggc	cgt	tta	gcg	aaa	cgc	ggc	gta	gct	gca	gtg	atg	cca	576	
Ile	Gly	His	Gly	Arg	Leu	Ala	Lys	Arg	Gly	Val	Ala	Ala	Val	Met	Pro		
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aca	ctt	gcc	gag	ttc	ccg	tat	gtg	gta	cgt	gtt	gtc	tct	gaa	atc	aca	624	
Thr	Leu	Ala	Glu	Phe	Pro	Tyr	Val	Val	Arg	Val	Val	Ser	Glu	Ile	Thr		
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Glu	Ser	Asn	Gly	Ser	Ser	Ser	Met	Ala	Ser	Val	Cys	Gly	Ala	Ser	Leu		
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Ala	Leu	Met	Asp	Ala	Gly	Val	Pro	Ile	Lys	Ala	Ala	Val	Ala	Gly	Ile		
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Ala	Met	Gly	Leu	Val	Lys	Glu	Asp	Glu	Lys	Phe	Val	Val	Leu	Ser	Asp		
			245					250						255			
atc	tta	ggc	gat	gaa	gat	cac	tta	ggc	gac	atg	gac	ttc	aaa	gtc	gcg	816	
Ile	Leu	Gly	Asp	Glu	Asp	His	Leu	Gly	Asp	Met	Asp	Phe	Lys	Val	Ala		
			260					265					270				
ggc	aca	cgt	acg	ggc	gtg	acg	gca	tta	caa	atg	gat	atc	aaa	atc	gaa	864	
Gly	Thr	Arg	Thr	Gly	Val	Thr	Ala	Leu	Gln	Met	Asp	Ile	Lys	Ile	Glu		
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Gly	Ile	Thr	Ala	Glu	Ile	Met	Gln	Ile	Ala	Leu	Asn	Gln	Ala	Lys	Ser		
	290				295						300						
gca	cgt	tta	cac	att	tta	ggc	gtg	atg	gag	caa	gcg	atc	cca	gcg	cca	960	
Ala	Arg	Leu	His	Ile	Leu	Gly	Val	Met	Glu	Gln	Ala	Ile	Pro	Ala	Pro		
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cgt	gcg	gat	att	tct	gat	ttt	gca	ccg	cgt	att	tac	act	atg	aaa	att	1008	
Arg	Ala	Asp	Ile	Ser	Asp	Phe	Ala	Pro	Arg	Ile	Tyr	Thr	Met	Lys	Ile		
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gat	ccg	aag	aaa	atc	aaa	gat	gtg	atc	ggc	aaa	ggc	ggc	gca	acc	att	1056	
Asp	Pro	Lys	Lys	Ile	Lys	Asp	Val	Ile	Gly	Lys	Gly	Gly	Ala	Thr	Ile		
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Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser
405 410 415

atc gta ggt aac aaa gaa ggc tta gtg cat att tct caa atc gcg gaa 1296
Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu
420 425 430

gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg ggg caa gaa gtg 1344
Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val
435 440 445

act gtt aaa gtg gtt gag att gat cgt caa ggt cgt att cgt tta acc 1392
Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr
450 455 460

atg aaa gaa gtt gca cca aag caa gaa cac gtt gat tct gtt gtc gca 1440
Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala
465 470 475 480

gac gtt gcc gca gaa gaa aac gca taagcaataa acaccaacgc ccttcgtgat 1494
Asp Val Ala Ala Glu Glu Asn Ala
485

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cagcttgtgt taatcatgaa caagtttttc tttcaaaaga gaaattaatg ttgacgagac 1674

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<213> Pasteurella multocida
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 50 55 60  
 Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile  
 65 70 75 80  
 Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr  
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 Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg  
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 Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala  
 115 120 125  
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 180 185 190  
 Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr  
 195 200 205  
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 210 215 220  
 Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile  
 225 230 235 240  
 Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp  
 245 250 255  
 Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala  
 260 265 270  
 Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu  
 275 280 285  
 Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn Gln Ala Lys Ser  
 290 295 300  
 Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro  
 305 310 315 320  
 Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile  
 325 330 335

Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile  
 340 345 350  
 Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp Ile Asp Asp Asp  
 355 360 365  
 Gly Thr Val Lys Ile Ala Val Asp Gly Asn Ser Ala Lys Glu Val  
 370 375 380  
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 385 390 395 400  
 Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser  
 405 410 415  
 Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu  
 420 425 430  
 Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val  
 435 440 445  
 Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr  
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 Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val  
 20 25 30  
 gtc att cct gtg cct gaa acc tct aac gat att gct tta cgt att gcg 145  
 Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala  
 35 40 45  
 cgc gtg tta aat aaa ccg tat cgt caa ggt ttt gtg aaa aat cgc tat 193  
 Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr  
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 65 70 75 80

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 145 150 155 160  
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 Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala  
 165 170 175  
 tta act ggt tct gtg caa caa gaa aat cca agt att caa gac ttt gat 577  
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 Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu  
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 Tyr Leu  
 210

&lt;210&gt; 46

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 46

Asp Gly Val Ser Val Tyr Ala Ala Arg Val His Met Gly Gln Arg Leu  
 1 5 10 15  
 Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val  
 20 25 30  
 Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala  
 35 40 45  
 Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr  
 50 55 60  
 Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser  
 65 70 75 80  
 Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn  
 85 90 95  
 Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln  
 100 105 110

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Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala
    115                      120                      125

Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met
    130                      135                      140

Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile
    145                      150                      155                      160

Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala
    165                      170                      175

Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp
    180                      185                      190

Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu
    195                      200                      205

Tyr Leu
    210

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&lt;210&gt; 47

&lt;211&gt; 4788

&lt;212&gt; DNA

&lt;213&gt; Pasteurella multocida

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (876)

&lt;220&gt;

&lt;223&gt; rci

&lt;220&gt;

&lt;223&gt; Nucleotide at position 3084 is A, T, G, or C.

&lt;400&gt; 47

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gac gag gag aga aaa tta gct gat ttg gca aaa ggt atc gct cca gat      48
Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys Gly Ile Ala Pro Asp
  1                      5                      10                      15

att att ttt aga gat gta ata gaa cgc tat caa aat gaa gtg tct ata      96
Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile
    20                      25                      30

act aaa aaa ggc gcg cga aat gaa att ata aga tta aac cgc ttt tta      144
Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu
    35                      40                      45

aga tat gat att tct aat ctg tat att cgt gat tta aga aaa gaa gat      192
Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp
    50                      55                      60

ttt gag gag tgg atc aga att cgc cta acc gaa gta tcg gat gct agc      240
Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser
    65                      70                      75                      80

gtt aga cgt gag ctt gtt act ata tcg tca gtg ctg aca aca gca ata      288
Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile
    85                      90                      95

aat aag tgg gga tat att tca agg cat cca atg act ggt att gaa aaa      336

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Asn	Lys	Trp	Gly	Tyr	Ile	Ser	Arg	His	Pro	Met	Thr	Gly	Ile	Glu	Lys	
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Pro	Lys	Asn	Ser	Ala	Glu	Arg	Lys	Glu	Arg	Tyr	Ser	Glu	Gln	Asp	Ile	
		115					120					125				
aaa	aca	ata	tta	gaa	aca	gct	aga	tat	tgt	gaa	gat	aaa	cta	ccc	ata	432
Lys	Thr	Ile	Leu	Glu	Thr	Ala	Arg	Tyr	Cys	Glu	Asp	Lys	Leu	Pro	Ile	
		130					135				140					
aca	ctc	aaa	caa	aga	gta	gca	att	gca	atg	tta	ttt	gct	att	gaa	acc	480
Thr	Leu	Lys	Gln	Arg	Val	Ala	Ile	Ala	Met	Leu	Phe	Ala	Ile	Glu	Thr	
		145				150				155					160	
gct	atg	cgt	gct	ggc	gag	att	gct	agt	ata	aaa	tgg	gat	aat	gtt	ttt	528
Ala	Met	Arg	Ala	Gly	Glu	Ile	Ala	Ser	Ile	Lys	Trp	Asp	Asn	Val	Phe	
				165					170					175		
ctt	gaa	aag	aga	ata	gta	cat	tta	ccg	aca	act	aaa	aac	ggg	cac	tct	576
Leu	Glu	Lys	Arg	Ile	Val	His	Leu	Pro	Thr	Thr	Lys	Asn	Gly	His	Ser	
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aga	gat	gtg	ccg	ctt	tcg	caa	aga	gct	gtt	gcg	cta	att	tta	aaa	atg	624
Arg	Asp	Val	Pro	Leu	Ser	Gln	Arg	Ala	Val	Ala	Leu	Ile	Leu	Lys	Met	
		195					200					205				
aaa	gag	gta	gaa	aat	gga	gat	ctt	gtg	ttt	cag	acc	acg	cct	gaa	tca	672
Lys	Glu	Val	Glu	Asn	Gly	Asp	Leu	Val	Phe	Gln	Thr	Thr	Pro	Glu	Ser	
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Leu	Ser	Thr	Thr	Phe	Arg	Val	Leu	Lys	Lys	Glu	Cys	Gly	Leu	Glu	His	
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ctc	cat	ttt	cat	gat	acg	aga	agg	gaa	gcg	ttg	acg	aga	tta	tct	aag	768
Leu	His	Phe	His	Asp	Thr	Arg	Arg	Glu	Ala	Leu	Thr	Arg	Leu	Ser	Lys	
				245					250					255		
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Lys	Val	Asp	Val	Met	Thr	Leu	Ala	Lys	Ile	Ser	Gly	His	Arg	Asp	Leu	
			260					265					270			
aga	att	tta	caa	aac	aca	tat	tac	gca	ccg	aat	atg	agt	gaa	gtg	gca	864
Arg	Ile	Leu	Gln	Asn	Thr	Tyr	Tyr	Ala	Pro	Asn	Met	Ser	Glu	Val	Ala	
		275					280					285				
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Asn	Leu	Leu	Asp													
		290														
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 aactaaaaac tctggtgccg gaatttcacg atctaataat ttctgttgca attcagtcac 4696  
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 aatttcagaa aaccagagtg gctctgcgaa tt 4788

&lt;210&gt; 48

&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 48

Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys Gly Ile Ala Pro Asp

1

5

10

15

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Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile
      20                      25                      30
Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu
      35                      40                      45
Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp
      50                      55                      60
Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser
      65                      70                      75                      80
Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile
      85                      90                      95
Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met Thr Gly Ile Glu Lys
      100                     105                     110
Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr Ser Glu Gln Asp Ile
      115                     120                     125
Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu Asp Lys Leu Pro Ile
      130                     135                     140
Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu Phe Ala Ile Glu Thr
      145                     150                     155                     160
Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys Trp Asp Asn Val Phe
      165                     170                     175
Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr Lys Asn Gly His Ser
      180                     185                     190
Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala Leu Ile Leu Lys Met
      195                     200                     205
Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln Thr Thr Pro Glu Ser
      210                     215                     220
Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu Cys Gly Leu Glu His
      225                     230                     235                     240
Leu His Phe His Asp Thr Arg Arg Glu Ala Leu Thr Arg Leu Ser Lys
      245                     250                     255
Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser Gly His Arg Asp Leu
      260                     265                     270
Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn Met Ser Glu Val Ala
      275                     280                     285
Asn Leu Leu Asp
      290

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<210> 49
<211> 1618
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (2)..(1195)

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&lt;223&gt; sopE

&lt;400&gt; 49

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 Gly Asp Leu Cys Leu Lys Ile Ser Thr Trp Cys Gln Ser His Arg Ile  
 1 5 10 15

aat caa gca att cgc aca att caa agt cta tca acc gca gtc atc ggt 97  
 Asn Gln Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly  
 20 25 30

att gtc tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat 145  
 Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn  
 35 40 45

gaa ccc gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga 193  
 Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ile Gly Lys Ala Gly  
 50 55 60

aaa caa ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc 241  
 Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val  
 65 70 75 80

aat tgc aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac 289  
 Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp  
 85 90 95

gaa gaa aca aaa gca agt gaa atg aac acg gca att att ggc aca atc 337  
 Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile  
 100 105 110

aca gaa gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa 385  
 Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys  
 115 120 125

aac aaa ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac 433  
 Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp  
 130 135 140

aca aaa gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac 481  
 Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn  
 145 150 155 160

gca ttt gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg 529  
 Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala  
 165 170 175

gtg caa tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg 577  
 Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met  
 180 185 190

ggc gat ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac 625  
 Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp  
 195 200 205

tat gcc gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa 673  
 Tyr Ala Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu  
 210 215 220

cag ggc tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc 721  
 Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser  
 225 230 235 240

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ggg gtc aca caa cca ctc tat ttt gac att aac gac agc tgc act gat 769
Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp
                245                250                255

gtg aac tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat 817
Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn
                260                265                270

ggc ttt cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc 865
Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe
                275                280                285

aag ttt gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att 913
Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile
                290                295                300

gca ggg cgc ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta 961
Ala Gly Ala Phe Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu
                305                310                315                320

gtg aaa gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc 1009
Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr
                325                330                335

aca aaa ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt 1057
Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu
                340                345                350

aac agt gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat 1105
Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp
                355                360                365

tat cac cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att 1153
Tyr His Pro Val Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile
                370                375                380

tct gat gaa tac ctt gtt gat ttt tca aat cgt tta gca tgc 1195
Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
                385                390                395

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tga 1618

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&lt;210&gt; 50

&lt;211&gt; 398

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 50

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 20 25 30  
 Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn  
 35 40 45  
 Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly  
 50 55 60  
 Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val  
 65 70 75 80  
 Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp  
 85 90 95  
 Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile  
 100 105 110  
 Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys  
 115 120 125  
 Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp  
 130 135 140  
 Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn  
 145 150 155 160  
 Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala  
 165 170 175  
 Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met  
 180 185 190  
 Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp  
 195 200 205  
 Tyr Ala Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu  
 210 215 220  
 Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser  
 225 230 235 240  
 Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp  
 245 250 255  
 Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn  
 260 265 270  
 Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe  
 275 280 285  
 Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile  
 290 295 300  
 Ala Gly Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu  
 305 310 315 320  
 Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr  
 325 330 335

Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu  
 340 345  
 Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp  
 355 360 365  
 Tyr His Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile  
 370 375 380  
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 385 390 395

<210> 51  
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<220>  
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 <222> (1)..(351)

<220>  
 <223> unknown C1

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 Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn  
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 Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe  
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 Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe  
 35 40 45  
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 Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys  
 50 55 60  
 gat agc tct aat ata cct ttg ttt agg agt aat tgg gaa ttg att atc 240  
 Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile  
 65 70 75 80  
 aat aat ata tat gat gtt gtc tgt tta tct aca aaa gta ttt ttt cta 288  
 Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu  
 85 90 95  
 gat gat gaa aag tta atg atg gaa tta ttt cct gaa gat aaa gta aga 336  
 Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg  
 100 105 110  
 gtc atc tat aaa aga ta 353  
 Val Ile Tyr Lys Arg  
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 <211> 117  
 <212> PRT  
 <213> *Pasteurella multocida*

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 Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe  
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 Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys  
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 Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile  
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 Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu  
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 Val Ile Tyr Lys Arg  
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 Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu  
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 cct tct tta tac ata gat tta att acg gcg cat aat gct ccg aag agt 144  
 Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser  
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 gaa gag aat tgc ttt gaa tat tac aat gag cgt aat gag ccc acg ttt 192  
 Glu Glu Asn Cys Phe Glu Tyr Tyr Asn Glu Arg Asn Glu Pro Thr Phe  
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 tct tcc ttt gga ttt gaa ggg ttt gag aca gag cgg tct agc gcc tct 240  
 Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Arg Ser Ser Ala Ser  
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 ctt gaa aat ata tat gct cag tat att tat gat gat cca atc tat ggt 288  
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 Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys  
 115 120 125

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<210> 54

<211> 169

<212> PRT

<213> Pasteurella multocida

<400> 54

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Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser  
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Glu Glu Asn Cys Phe Glu Tyr Tyr Asn Glu Arg Asn Glu Pro Thr Phe  
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Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Arg Ser Ser Ala Ser  
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Leu Glu Asn Ile Tyr Ala Gln Tyr Ile Tyr Asp Asp Pro Ile Tyr Gly  
 85 90 95

Tyr Glu His Val Tyr Ser Phe Gly Ser Thr Gly Glu Gly His Phe Ile  
 100 105 110

Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys  
 115 120 125

Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu  
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Phe Asp Glu Met Ile Glu Lys Tyr Ser  
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<210> 55

<211> 443

&lt;212&gt; DNA

&lt;213&gt; Pasteurella multocida

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(441)

&lt;220&gt;

&lt;223&gt; unknown C3

&lt;400&gt; 55

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Ser	Ser	Asp	Phe	Glu	Val	Asp	Glu	Leu	Ser	His	Lys	Asp	Glu	His	Glu	
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Val	Asp	Asn	Tyr		Phe	Ser	Cys	Pro	Phe	Ile	His	Glu	Leu	Ile	Cys	
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Pro	Asn	Phe	Lys	Gly	Ser	Gly	Trp	Val	Arg	Tyr	Ser	Tyr	Asn	Gly	Arg	
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aat	att	cat	ttc	gaa	ttt	aat	gaa	tct	aat	gaa	tta	tcc	cag	att	agc	432
Asn	Ile	His	Phe	Glu	Phe	Asn	Glu	Ser	Asn	Glu	Leu	Ser	Gln	Ile	Ser	
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Ile	Phe	Ile														
145																

&lt;210&gt; 56

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 56

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      65              70              75              80
Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp
      85              90              95
Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu
      100             105             110
Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg
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Tyr Leu Ile Arg Ser Cys Tyr Asp Ser Val Arg Lys Phe Tyr Glu Asn
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Glu Leu Gly Val Tyr Thr Val Met Thr Ala Leu Leu Ala Phe Pro Leu
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Lys Ala Arg Leu Ala Gln Gly Met Asp Gln Ala Ala Leu Ala Leu Val
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Ala Glu Asn Asn Asp Tyr Arg Glu Asn Lys Lys His Gly Asp Val Asn
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Thr	Gly	Asn	Asn	Thr	Pro	Trp	Lys	Phe	Asn	Ala	Gly	Arg	Trp	Glu	Arg	
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agt	aca	gtg	tct	ttc	cag	gag	cat	tat	aaa	ggc	tat	tat	gac	aaa	ttc	3705
Ser	Thr	Val	Ser	Phe	Gln	Glu	His	Tyr	Lys	Gly	Tyr	Tyr	Asp	Lys	Phe	
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His Ser Ser Thr Cys Arg Gly Ser Gly Ser Ser Arg Thr Cys Gln Ile	
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Asp Ala Asn Pro Lys Lys Ile Met Asp Tyr Ala Leu Lys Ile Asn Asp	
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Trp Thr Thr Ile Arg Glu Leu Phe Asn Thr Tyr Ile Asp Val Ser Gly	
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Thr Ile Asp Gln Ile Ser Gln Phe Asp Gly Ser Asn Arg Arg Tyr Asp	
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Asp Ser Phe Lys Gln Ile Ile Gly Phe Glu Glu Val Gly Arg Ser	
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Val Ser Glu Ser Leu Val Ser Glu Asp Lys Leu Lys Lys Asp Arg Val		
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Glu Asp Val Ser Glu Gly Val Ser Pro Phe Asn Arg Ile Gly Phe Thr		
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Leu Pro Tyr Glu Gly Lys Ile Ser Gln Thr Ser Arg Lys Leu Thr Ile		
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Arg Tyr Trp Ile Thr Gly Asn Asn Thr Pro Trp Lys Phe Asn Ala Gly		
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Arg Trp Glu Arg Ser Thr Val Ser Phe Gln Glu His Tyr Lys Gly Tyr		
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Tyr Asp Lys Phe His Ser Ser Thr Cys Arg Gly Ser Gly Ser Ser Arg		
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Thr Cys Gln Ile Asp Ala Asn Pro Lys Lys Ile Met Asp Tyr Ala Leu		
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Ala Ser Ser Gly Leu Leu Val Gly Ala Asn Ile Met Met Asp Glu Asn
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Lys Asn Pro Asp Ala Gln Pro Ser Lys Leu Gly Thr Asn Ile Gln Arg
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Val Ile Leu Val Leu Ser Asp Gly Glu Asp Asn Trp Pro Thr Tyr Ser
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Thr Leu Thr Thr Leu Leu Asn Asn Gly Met Cys Asp Lys Ile Arg Glu
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Gln Leu Gly Lys Leu Gln Asp Pro Asn Leu Arg Glu Leu Pro Gly Arg
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Ile Ala Phe Val Ala Phe Gly Tyr Ser Pro Pro Ala Asn Gln Val Ala
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Ala Trp Lys Lys Cys Val Gly Asp Gln Tyr Tyr Thr Ala Tyr Ser Lys
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acc cat tct cag caa ggc atg aca cag aaa agt atg tca tct gaa aca 811  
Thr His Ser Gln Gln Gly Met Thr Gln Lys Ser Met Ser Ser Glu Thr  
25 30 35  
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Ile Arg Tyr Lys Leu Ala Lys Thr Tyr Tyr Gln Arg Gly Asp Ser Lys  
75 80 85  
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Ser Ser Leu Leu Tyr Leu Thr Pro Leu Leu Asn Asp Asn Thr Lys Leu  
90 95 100  
gct aca caa cgc aaa ata tta cag ata aaa aat cta att caa tta aat 1051  
Ala Thr Gln Ala Lys Ile Leu Gln Ile Lys Asn Leu Ile Gln Leu Asn  
105 110 115  
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Asn Phe Gln Glu Ala Ile Ser Val Ala Asn Glu Leu Leu Lys Ser  
120 125 130  
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Pro Asn Glu Gly Glu Val Tyr Asn Leu Arg Gly Ile Ala Tyr Ala Gln  
135 140 145 150  
aat ggg aat ttg gtg aat gcc cga aat gat atc aat aaa gca aga gag 1195  
Asn Gly Asn Leu Val Asn Ala Arg Asn Asp Ile Asn Lys Ala Arg Glu  
155 160 165  
ttc ttt att aat gat aat gtt gct att aat aat tta gcc atg cta aat 1243  
Phe Phe Ile Asn Asp Asn Val Ala Ile Asn Asn Leu Ala Met Leu Asn  
170 175 180  
att att aat ggc gat ttt aat aat gct gtt tct tta ctg ttg cca caa 1291  
Ile Ile Asn Gly Asp Phe Asn Asn Ala Val Ser Leu Leu Pro Gln  
185 190 195  
tat tta aat ggc gtt aag aat tct cga ttg att cat aat ctt gtt ttt 1339

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Tyr Leu Asn Gly Val Lys Asn Ser Arg Leu Ile His Asn Leu Val Phe
200                               205                               210

gct tta gtt aaa aat ggt gat ctt gat tat gca aaa gat atc att gtt 1387
Ala Leu Val Lys Asn Gly Asp Leu Asp Tyr Ala Lys Asp Ile Ile Val
215                               220                               230

aaa gag cgt tta aat act tca cca gat gat tta att aat gca ttg aaa 1435
Lys Glu Arg Leu Asn Thr Ser Pro Asp Asp Leu Ile Asn Ala Leu Lys
235                               240                               245

aaa act aca cat gta tca aaa ggt gta act cgg taacactaag gatttgatat 1488
Lys Thr Thr His Val Ser Lys Gly Val Thr Arg
250                               255

gaaaaagtgt ctatcaata taaaaggaa ctcgtcaatt gaatttgctt tgacgatagc 1548
gttctatttta ttgttgtga tgtttatttt tgaattttgt cgatttagcgg ttgcgacagc 1608
ttattgggat ttactataa cggaaagtgt cagaattgag aagaatgaac aagcaatttc 1668
tggaattatt gaagaagcat ttaggaaagc tcttacaag caaaaaaat tccatgatga 1728
atcgacaatt ggtattttgg cgttgttaga agataataaa ttgatgtaa aagtccaata 1788
tgtggattgt gataaagaaa cggaaatgtat taaaaatctt ctgcttaata aatttcgcca 1848
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acaattattct ttaactata aatataagtt tatggtgcgg ttagatttta ttcttgagtc 1968
ttggtctcaa gtagtgtga accgtgaatt tgttgttga caggaaattg agcgttctca 2028
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gatgttaatc ggcaagtagt atcgctcaa gacaaagcaa aatttgggtg taatgaattt 2988  
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&lt;210&gt; 61

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 61

Met	Phe	Phe	Lys	Phe	Thr	Lys	Lys	Ile	Val	Phe	Val	Ser	Leu	Ala	Leu
1				5					10					15	
Ser	Val	Val	Gly	Cys	Ser	Thr	His	Ser	Gln	Gln	Gly	Met	Thr	Gln	Lys
			20				25						30		
Ser	Met	Ser	Ser	Glu	Thr	Ile	Thr	Ala	Lys	Glu	Thr	Leu	Tyr	Glu	Ser
			35				40					45			
Thr	Gln	Asn	Tyr	Ser	Ala	Leu	Ile	Ser	Leu	Tyr	Arg	Asp	Val	Leu	Lys
		50					55				60				
Ala	Lys	Glu	Asp	Pro	Ser	Ile	Arg	Tyr	Lys	Leu	Ala	Lys	Thr	Tyr	Tyr
		65				70				75				80	
Gln	Arg	Gly	Asp	Ser	Lys	Ser	Ser	Leu	Leu	Tyr	Leu	Thr	Pro	Leu	Leu
			85					90						95	
Asn	Asp	Asn	Thr	Lys	Leu	Ala	Thr	Gln	Ala	Lys	Ile	Leu	Gln	Ile	Lys
			100					105					110		
Asn	Leu	Ile	Gln	Leu	Asn	Asn	Phe	Gln	Glu	Ala	Ile	Ser	Val	Ala	Asn
			115					120				125			

Glu Leu Leu Leu Lys Ser Pro Asn Glu Gly Glu Val Tyr Asn Leu Arg  
 130 135 140  
 Gly Ile Ala Tyr Ala Gln Asn Gly Asn Leu Val Asn Ala Arg Asn Asp  
 145 150 155 160  
 Ile Asn Lys Ala Arg Glu Phe Phe Ile Asn Asp Asn Val Ala Ile Asn  
 165 170 175  
 Asn Leu Ala Met Leu Asn Ile Ile Asn Gly Asp Phe Asn Asn Ala Val  
 180 185 190  
 Ser Leu Leu Leu Pro Gln Tyr Leu Asn Gly Val Lys Asn Ser Arg Leu  
 195 200 205  
 Ile His Asn Leu Val Phe Ala Leu Val Lys Asn Gly Asp Leu Asp Tyr  
 210 215 220  
 Ala Lys Asp Ile Ile Val Lys Glu Arg Leu Asn Thr Ser Pro Asp Asp  
 225 230 235 240  
 Leu Ile Asn Ala Leu Lys Lys Thr Thr His Val Ser Lys Gly Val Thr  
 245 250 255

Arg

<210> 62  
 <211> 1788  
 <212> DNA  
 <213> *Pasteurella multocida*

<220>  
 <221> CDS  
 <222> (1)..(600)

<220>  
 <223> unknown K

<400> 62  
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 Val Asn Thr Gly Leu Ile His Ser Asn Gly Asn Ala Lys Leu Thr Phe  
 1 5 10 15  
 aaa gat gac acc agt ttt gtg act gaa gga aat aac ttt atc aca gca 96  
 Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala  
 20 25 30  
 aaa gac aac tta gaa atc acg gca aaa aat gtt caa att gat caa gcg 144  
 Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala  
 35 40 45  
 aaa aat att caa tta aac gcg aat atc acg atc aat acc aag tct ggt 192  
 Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly  
 50 55 60  
 ttt gtg aat tac ggt acc tta gca agt gct caa aat tta acg att aat 240  
 Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn  
 65 70 75 80  
 acc gaa caa ggc agc att tat aac ata ggc ggt atc ttg ggg gcg ggt 288  
 Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly

	85	90	95	
aaa agt ttg aat ctg agc gcg aaa aga gga gaa aac caa gga gga tat				336
Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr	100	105	110	
ctt att aat caa ggt aag agt cta ctc cat tct gaa ggc gcc atg aac				384
Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn	115	120	125	
ctc aca gcg gat cgc acg gty tac aat tta ggg aat att ttt gct aaa				432
Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys	130	135	140	
ggt gac gcg acg atc aat gca aac gcg tta att aat gat gtt act ctc				480
Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu	145	150	155	
aca ggt cgt ctt gag tat caa gat ctg aaa aaa gat tat acg cgt tat				528
Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr	165	170	175	
tat cgt atc aat gaa acg gca aaa cat ggt tgg cat aat aac ttc tat				576
Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr	180	185	190	
gaa tta aac gtc gac aga gtt tct tgatttgcgc atcaattttg taaccacogg				630
Glu Leu Asn Val Asp Arg Val Ser	195	200		
ttaataaaac accagcaatt tcaacgccat tcatggcaga taatgccgct gcgacgatca				690
catcaggacg atccgcggaa gtgacaagta aacttccaac gcggaaatgt tccaccatat				750
tggtcaaat acgtgcacag aaagtgatgc cagcaatgcg acgttcattg atcgcgcctt				810
catgaataat ggcagcacct aaatgttttg ctaaatcaat ggcacgagtc gcaattaatt				870
ctgcgctcca aggaatacat gccagattt taattgggct tttctcaaat aaatgataaa				930
tctcagatac ttgattttgt gtgtgttgga aagaatcaaa aatttctgcc aagtcagggc				990
gagtagcacc agattcatca atcggcgcat taaatttatt gatcacaaca ccaagtaaat				1050
tagggttatt tttgctgcca aataatgagg ctgcgggttt gatgcgttct ttgagttctg				1110
ccggtgtttc cgtcgcgggt gctgcaacaa gaatgatttc cgcatacagt gcttgagcaa				1170
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cgacaatttc attgtttttg gcgagtgttt gatgattttc aacaattttt tctagtagca				1290
catcagattg attttgaccg atgagtgatt cagctacact taacataaat ggttcaactg				1350
tttcaatggt ggtactggtg cgaataattg atgttgtgcg atcaatcata tcttcaacct				1410
agttcggtg agaatttggt ttcataaagc cgacttttgc ccctttttgc tccagtgcat				1470
gtgttaaacc taagctgaca ctgggtaagc ctacaccagc actaatcggg ataaggataa				1530
ttgtacgtga cataataaac cctaattttg tgataattta tacaaaaaga aactgccgat				1590
gaatcggcag ttaattgatc tttacgcgat gcaaaggcgc gcggtattct gtgcataaac				1650

aagttcttca ttcgttgga tcaccatggc aacagcgcta ttgtctgtg taatcacccc 1710  
 ttcattgacca aagcgagcgg ctttgttttt atctgaatcc acttgataac cgaacagttt 1770  
 taaatggttt aaggttga 1788

<210> 63  
 <211> 200  
 <212> PRT  
 <213> *Pasteurella multocida*

<400> 63  
 Val Asn Thr Gly Leu Ile His Ser Asn Gly Asn Ala Lys Leu Thr Phe  
 1 5 10 15  
 Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala  
 20 25 30  
 Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala  
 35 40 45  
 Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly  
 50 55 60  
 Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn  
 65 70 75 80  
 Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly  
 85 90 95  
 Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr  
 100 105 110  
 Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn  
 115 120 125  
 Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys  
 130 135 140  
 Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu  
 145 150 155 160  
 Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr  
 165 170 175  
 Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr  
 180 185 190  
 Glu Leu Asn Val Asp Arg Val Ser  
 195 200

<210> 64  
 <211> 278  
 <212> DNA  
 <213> *Pasteurella multocida*

<220>  
 <221> CDS  
 <222> (108)..(278)  
 <220>

&lt;223&gt; unknown O

&lt;400&gt; 64

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cattacccaa atggaaataa accttaacca tagcaagaga gaagaaa atg aaa att 116
                                     Met Lys Ile
                                     1
act att aca cga aat cat cca gaa gta ttt caa gaa tcc gct cgt tta 164
Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser Ala Arg Leu
      5                10                15
gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca tta aca ttg 212
Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala Leu Thr Leu
      20                25                30                35
gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt gag gag gaa 260
Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly Glu Glu Glu
                40                45                50
agc aaa agg gga cat agt 278
Ser Lys Arg Gly His Ser
                55

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&lt;210&gt; 65

&lt;211&gt; 57

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 65

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Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
      1                5                10                15
Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
                20                25                30
Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
                35                40                45
Glu Glu Glu Ser Lys Arg Gly His Ser
      50                55

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&lt;210&gt; 66

&lt;211&gt; 1020

&lt;212&gt; DNA

&lt;213&gt; Pasteurella multocida

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(597)

&lt;220&gt;

&lt;223&gt; unknown P

&lt;400&gt; 66

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gtc aac aca tca aaa gtt gag att gac tat gcc gtc act cgt gcg gcg 48
Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala
      1                5                10                15
gca atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att 96

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Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile  
20 25 30

tca aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat 144  
Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr  
35 40 45

ttt gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa 192  
Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln  
50 55 60

ggc atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta 240  
Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu  
65 70 75 80

cgc acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc 288  
Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg  
85 90 95

act gca caa atc tta aaa gat acg att gca ggg cgc ttt gat tgg gca 336  
Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala  
100 105 110

gtg gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca 384  
Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala  
115 120 125

atc aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc 432  
Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly  
130 135 140

ggt aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa 480  
Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys  
145 150 155 160

gat gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc 528  
Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu  
165 170 175

gaa cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat 576  
Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp  
180 185 190

ttt tca aat cgt tta gca tcg taagggttag aaaatggcctt taccacgcaa 627  
Phe Ser Asn Arg Leu Ala Ser  
195

acttaaatg atgaatttaa tcatcgacgg taacaaatat ctgcgcgaag tcacggaagt 687

gactcaacca aaattagcaa tgaaaatcga agaatttcgc gcgggcggta tgattggttc 747

gggtgatgtc aatctcgggc ttgaaaagct cgaagcggaa tttaaagccg gtggctacat 807

ggtcgaatta attaaaaaat tcggcgggtc aatcaacggc attccattgc gttttcttgg 867

ctcatatcag cgtgatgaca cagaagaagt cacatctggt gagcttgta tgcaaggtcg 927

atttactgaa attgacagcg gaaacagcaa agtgggcgat gacactgaac aaacattcaa 987

agtgccttta acgtattaca aaatcattgt tga 1020

&lt;210&gt; 67

&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 67

Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala  
 1 5 10 15

Ala Met Arg Ala Tyr Leu Asp Lys Glu Gly Trp His Thr Ser Ile  
 20 25 30

Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr  
 35 40 45

Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln  
 50 55 60

Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu  
 65 70 75 80

Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg  
 85 90 95

Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala  
 100 105 110

Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala  
 115 120 125

Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly  
 130 135 140

Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys  
 145 150 155 160

Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu  
 165 170 175

Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp  
 180 185 190

Phe Ser Asn Arg Leu Ala Ser  
 195

&lt;210&gt; 68

&lt;211&gt; 2584

&lt;212&gt; DNA

&lt;213&gt; Pasteurella multocida

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1042)..(2286)

&lt;220&gt;

&lt;223&gt; xylA

&lt;400&gt; 68

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 cgcgatggtc tttttgggtc ttatttacgt gctgttttagc agtattgtgg catttaaaat 180



tgg ggg act gca aat tgt ttt aca cac cct cgt tat atg tct ggt gct Trp Gly Thr Ala Asn Cys Phe Thr His Pro Arg Tyr Met Ser Gly Ala 140 145 150	1503
gca aca aat ccg aat cca gaa att ttt gct tgg gct gct gca caa gta Ala Thr Asn Pro Asn Pro Glu Ile Phe Ala Trp Ala Ala Ala Gln Val 155 160 165 170	1551
ttt act gcc atg ggg gca act cag cgt tta ggt ggt gaa aat tat gtt Phe Thr Ala Met Gly Ala Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val 175 180 185	1599
ttg tgg gga gga cgt gaa gga tat gaa acg tta tta aat acc aat tta Leu Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu 190 195 200	1647
aaa cag gag cga gag caa att gga cgt ttc atg caa atg gtg gtt gag Lys Gln Glu Arg Glu Gln Ile Gly Arg Phe Met Gln Met Val Val Glu 205 210 215	1695
cat aaa tat aaa atc ggt ttt aac ggg act ttg ctg att gaa cca aag His Lys Tyr Lys Ile Gly Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys 220 225 230	1743
cca caa gag cca acg aaa cat caa tat gac tat gat gtg gcg acc gtt Pro Gln Glu Pro Thr Lys His Gln Tyr Asp Tyr Asp Val Ala Thr Val 235 240 245 250	1791
tat gcc ttt tta aag cag ttt ggt tta gaa gaa att aaa gtg aat Tyr Gly Phe Leu Lys Gln Phe Gly Leu Glu Lys Glu Ile Lys Val Asn 255 260 265	1839
att gaa gct aat cac gca aca tta gct gga cac act ttc cag cat gaa Ile Glu Ala Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Gly 270 275 280	1887
gtc gcc atg gct aca gcg tta gat att ttt ggt tct att gat gca aat Val Ala Met Ala Thr Ala Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn 285 290 295	1935
cgt ggt gat cca caa tta ggt tgg gat acc gat caa ttc cct aat agc Arg Gly Asp Pro Gln Leu Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser 300 305 310	1983
gta gaa gaa aat act ttg gtc ata tat gaa att ctg aaa gca ggg ggc Val Glu Glu Asn Thr Leu Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly 315 320 325 330	2031
ttt aca acc ggt ggt ttt aat ttt gat gct aaa atc cgt cgg cag agt Phe Thr Thr Gly Gly Phe Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser 335 340 345	2079
acg gat cct tac gat tta ttt cat gga cat att ggc gcg att gat gta Thr Asp Pro Tyr Asp Leu Phe His Gly His Ile Gly Ala Ile Asp Val 350 355 360	2127
ctt gcc tta tca cta aaa tgt gcg gcg aaa atg ctt gaa gag caa gct Leu Ala Leu Ser Leu Lys Cys Ala Ala Lys Met Leu Glu Glu Gln Ala 365 370 375	2175
tta caa aaa gtc gtc aat caa cgt tat gct ggt tgg aca tca tca ctt Leu Gln Lys Val Val Asn Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu 380 385 390	2223

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ggt caa ctt gtt caa atc cgg tcc tac cac gcg tgt ctg caa tac aga 2271
Gly Gln Leu Val Gln Ile Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg
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cta aca aaa gtg ctt taaaacgttc cggttacgc cagacatcta gacgattgaa 2326
Leu Thr Lys Val Leu
          415

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acaacaaagt tctgcaaaat cttgaattgc gtgaggtaat ttaaagcgcg gacataagcg 2446

tcttgcgcgc atgacaccag ctttttcatg tccataatga tgtggcaata tttcttttgg 2506

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gtcgtgtgtt tctgtcga
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<210> 69
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<212> PRT
<213> Pasteurella multocida

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Thr Ser Ser Asn Pro Phe Ala Tyr Lys His Tyr Asp Ala Asn Gln Val
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Ile Leu Gly Lys Thr Met Ala Glu His Leu Arg Leu Ala Val Cys Tyr
          35          40          45

Trp His Thr Phe Cys Trp Thr Gly Asn Asp Met Phe Gly Val Gly Ser
          50          55          60

Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp Ser Leu Ala Gly Ala Lys
          65          70          75          80

Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe Ser Lys Leu Gly Ile Pro
          85          90          95

Tyr Tyr Cys Phe His Asp Val Asp Val Ala Pro Glu Gly His Ser Phe
          100          105          110

Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met Ile Asp Val Leu Ala Gln
          115          120          125

Lys Gln Glu Glu Thr Gly Val Lys Leu Leu Trp Gly Thr Ala Asn Cys
          130          135          140

Phe Thr His Pro Arg Tyr Met Ser Gly Ala Ala Thr Asn Pro Asn Pro
          145          150          155          160

Glu Ile Phe Ala Trp Ala Ala Ala Gln Val Phe Thr Ala Met Gly Ala
          165          170          175

Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val Leu Trp Gly Gly Arg Glu
          180          185          190

Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu Lys Gln Glu Arg Glu Gln
          195          200          205

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Ile Gly Arg Phe Met Gln Met Val Val Glu His Lys Tyr Lys Ile Gly  
 210 215 220  
 Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys Pro Gln Glu Pro Thr Lys  
 225 230 235 240  
 His Gln Tyr Asp Tyr Asp Val Ala Thr Val Tyr Gly Phe Leu Lys Gln  
 245 250 255  
 Phe Gly Leu Glu Lys Glu Ile Lys Val Asn Ile Glu Ala Asn His Ala  
 260 265 270  
 Thr Leu Ala Gly His Thr Phe Gln His Glu Val Ala Met Ala Thr Ala  
 275 280 285  
 Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn Arg Gly Asp Pro Gln Leu  
 290 295 300  
 Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser Val Glu Glu Asn Thr Leu  
 305 310 315 320  
 Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly Phe Thr Thr Gly Gly Phe  
 325 330 335  
 Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser Thr Asp Pro Tyr Asp Leu  
 340 345 350  
 Phe His Gly His Ile Gly Ala Ile Asp Val Leu Ala Leu Ser Leu Lys  
 355 360 365  
 Cys Ala Ala Lys Met Leu Glu Glu Gln Ala Leu Gln Lys Val Val Asn  
 370 375 380  
 Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu Gly Gln Leu Val Gln Ile  
 385 390 395 400  
 Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg Leu Thr Lys Val Leu  
 405 410 415

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 <212> DNA  
 <213> Pasteurella multocida

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 <222> (298)..(1905)

<220>  
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 gtcaagaata atgtgatgtt accggtgatt aataccaata ttgaaccgca ctttgatgcc 180  
 cttagagcca cccaaatgaa cagcaaagtg ctcgatacct caaaagtgaa tgccgaacaa 240  
 gtcaaaaat ggattgctgt ttggcaaacg accctaacc aataattgtt tgtcttg 297

atg ttt aag cga ttt cgt gca ttc aca tac cgt ccc gcc agt tat ctt Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu	345
1 5 10 15	
ggc ggg atg ttg gtg att gtt ttt ctg agc gct ttt tat gcg ttc gcc Gly Gly Met Leu Val Ile Val Phe Leu Ser Ala Phe Tyr Ala Phe Ala	393
20 25 30	
tta ggg gcg gtt ttt tcg ctc cct ttt gcg cgc agt tgg aca gcg ttg Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Trp Ala Leu	441
35 40 45	
ttg agt gat cag tat tta caa cac gtg atc atc ttt agc ttt tgg caa Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln	489
50 55 60	
gcc ttt ctg tcg gcg gta ctt gcg gtc ctc ttt ggt gcc att gta gca Ala Phe Leu Ser Ala Val Leu Ala Val Leu Phe Gly Gly Ile Val Ala	537
65 70 75 80	
cga gcc ttt ttt tat caa ccg ttt gtg gcc aag aaa ctg atc ctc aaa Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys	585
85 90 95	
tta ttt tca ctg act ttt gtg tta cct gcc tta gtg gcg att ttt ggt Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly	633
100 105 110	
tta tta ggc gtg tat ggc gct tct ggc tgg tta gcg atg tta agc cag Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln	681
115 120 125	
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130 135 140	
tta ctg gcg cat ctt ttt ttt aat gtc cca tta gct tgt cgc ctg ttt Leu Leu Ala His Leu Phe Phe Asn Val Pro Leu Ala Cys Arg Leu Phe	777
145 150 155 160	
tta caa ggt ttg caa gca att ccg gtg caa caa cgt cag ctc gcg gca Leu Gln Gly Leu Gln Ala Ile Pro Val Gln Gln Arg Gln Leu Ala Ala	825
165 170 175	
caa ctc aat tta cgt ggt tgg cat ttt ata cgt ctg att gag tgg ccc Gln Leu Asn Leu Arg Gly Trp His Phe Ile Arg Leu Ile Glu Trp Pro	873
180 185 190	
tat tta cgc cag caa ttg tta cct gca ttt act ttg att ttc atg ctg Tyr Leu Arg Gln Gln Leu Leu Pro Ala Phe Thr Leu Ile Phe Met Leu	921
195 200 205	
tgt ttt acc agt ttt gcg att gtg ctc act tta ggt gcc gga ccg aaa Cys Phe Thr Ser Phe Ala Ile Val Leu Thr Leu Gly Gly Pro Lys	969
210 215 220	
tat acc acg ttg gaa gtg gct atc tat caa gcg att tta ttt gag ttt Tyr Thr Thr Leu Glu Val Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe	1017
225 230 235 240	
gat gta ccg aaa gcc ggc tta ttt gcg tta tta caa ttt gtt ttt tgt Asp Val Pro Lys Ala Gly Leu Phe Ala Leu Leu Gln Phe Val Phe Cys	1065
245 250 255	

ttt ctg tta	ttc acg ctg agt agc ttt ttt tct cca gcc ccc gcc acg	1113
Phe Leu Leu	Phe Thr Leu Ser Ser Phe Phe Ser Pro Ala Pro Ala Thr	
	260 265 270	
aca tta cac	agt caa cct act tgg ttt gcg ccc caa tgg tat tgg gtt	1161
Thr Leu His	Ser Gln Pro Thr Trp Phe Ala Pro Gln Ser Tyr Trp Val	
	275 280 285	
aaa tta tgg	caa cgt atg atc att gtg tgt gcg aca gta ttt atc tta	1209
Lys Leu Trp	Gln Arg Met Ile Ile Val Cys Ala Thr Val Phe Ile Leu	
	290 295 300	
tta cgg cta	ctc aat acg cta gtt tct gct ttg ctt tgg tct cag ttt	1257
Leu Pro Leu	Leu Asn Thr Leu Val Ser Ala Leu Leu Ser Ser Gln Phe	
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ttt acc ttg	tgg tta caa cct caa tta tgg aaa gca tta ggt tac tgg	1305
Phe Thr Leu	Trp Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser	
	325 330 335	
ctc acc atc	gcc ccc act tct gca ttg ctg gct tta gta ctg tct ttt	1353
Leu Thr Ile	Ala Pro Thr Ser Ala Leu Leu Ala Leu Val Ser Phe	
	340 345 350	
gcc tta tta	ttg ctt gcc aga gaa tta cat tgg cga cat tat cgc agc	1401
Ala Leu Leu	Leu Leu Ala Arg Glu Leu His Trp Arg His Tyr Arg Ser	
	355 360 365	
tta tcc cat	gtg att tta aat atc ggt gcg acc att tta gcc att cca	1449
Leu Ser His	Val Ile Leu Asn Ile Gly Ala Thr Ile Leu Ala Ile Pro	
	370 375 380	
acg tta gtg	tta gct att ggt tta ttc att tta tta cgt gag atc gat	1497
Thr Leu Val	Leu Ala Ile Gly Leu Phe Ile Leu Leu Arg Glu Ile Asp	
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ttt tct cca	tac cat ctt ttt ggg gtt gtg gta tgc tgt aac gcg tta	1545
Phe Ser Pro	Tyr His Leu Phe Gly Val Val Val Cys Cys Asn Ala Leu	
	405 410 415	
gct gct atg	cct ttt gtg ttg cgt att ttg gct tta ccg atg cat aac	1593
Ala Ala Met	Pro Phe Val Leu Arg Ile Leu Ala Leu Pro Met His Asn	
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aat atg att	tat tat gaa aaa tta tgc caa tca ctt aac ctg cgt ggt	1641
Asn Met Ile	Tyr Tyr Glu Lys Leu Cys Gln Ser Leu Asn Leu Arg Gly	
	435 440 445	
tgg caa cgt	ttt cga ttg att gaa tgg cac aag ctt cgt gcg cca atg	1689
Trp Gln Arg	Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met	
	450 455 460	
aaa tac gcc	ttt gca ctg gct tgt gcg tta tca tta ggc gat ttc acc	1737
Lys Tyr Ala	Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr	
	465 470 475 480	
gca atc gcg	tta ttt ggt cag gct gac ttc aca tgg tta ccg cat ttg	1785
Ala Ile Ala	Leu Phe Gly Gln Ala Asp Phe Thr Ser Leu Pro His Leu	
	485 490 495	
ttg tat caa	caa ttg ggg cat tat cgt agt cag gaa gcg gca gta aca	1833
Leu Tyr Gln	Gln Leu Gly His Tyr Arg Ser Gln Glu Ala Ala Val Thr	
	500 505 510	

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gcg ttt att tta ttg gtt ttt tgt ttg agt gtt ttt atg att att gaa 1881
Ala Phe Ile Leu Leu Val Phe Cys Leu Ser Val Phe Met Ile Ile Glu
      515                      520                      525

cga cat cag gaa cgg cgt gat gat taatttaaac ggtgttcagt ttccctataa 1935
Arg His Gln Glu Pro Arg Asp Asp
      530                      535

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3501

<210> 71  
 <211> 536  
 <212> PRT  
 <213> Pasteurella multocida

<400> 71

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      20             25             30

Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Thr Ala Leu
      35             40             45

Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln
      50             55             60

Ala Phe Leu Ser Ala Val Leu Ala Val Leu Phe Gly Gly Ile Val Ala
      65             70             75             80

Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys
      85             90             95

Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly
      100            105            110

Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln
      115            120            125

Phe Phe Ala Trp Asp Trp Thr Pro Asn Ile Tyr Gly Leu Thr Gly Ile
      130            135            140

Leu Leu Ala His Leu Phe Phe Asn Val Pro Leu Ala Cys Arg Leu Phe
      145            150            155            160

Leu Gln Gly Leu Gln Ala Ile Pro Val Gln Gln Arg Gln Leu Ala Ala
      165            170            175

Gln Leu Asn Leu Arg Gly Trp His Phe Ile Arg Leu Ile Glu Trp Pro
      180            185            190

Tyr Leu Arg Gln Gln Leu Leu Pro Ala Phe Thr Leu Ile Phe Met Leu
      195            200            205

Cys Phe Thr Ser Phe Ala Ile Val Leu Thr Leu Gly Gly Gly Pro Lys
      210            215            220

Tyr Thr Thr Leu Glu Val Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe
      225            230            235            240

Asp Val Pro Lys Ala Gly Leu Phe Ala Leu Leu Gln Phe Val Phe Cys
      245            250            255

Phe Leu Leu Phe Thr Leu Ser Ser Phe Phe Ser Pro Ala Pro Ala Thr
      260            265            270

Thr Leu His Ser Gln Pro Thr Trp Phe Ala Pro Gln Ser Tyr Trp Val
      275            280            285

Lys Leu Trp Gln Arg Met Ile Ile Val Cys Ala Thr Val Phe Ile Leu
      290            295            300
  
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Leu Pro Leu Leu Asn Thr Leu Val Ser Ala Leu Leu Ser Ser Gln Phe  
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 Phe Thr Leu Trp Leu Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser  
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 Ala Leu Leu Leu Leu Ala Arg Glu Leu His Trp Arg His Tyr Arg Ser  
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 Phe Ser Pro Tyr His Leu Phe Gly Val Val Cys Cys Asn Ala Leu  
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 465 470 475 480  
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 485 490 495  
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gagaagcatt atttactcca tcaggaaaaa tcaaatgca aacttctgga agtgtattag 1500
acatgccatt tccagcaatt gaaaaaagtt tcttctttat ttc atg cct cat cat 1555
                               Met Pro His His
                               1

tgt tgt tct ttc agt act aca tat att ccg tca cat cta tac aaa ata 1603
Cys Cys Ser Phe Ser Thr Thr Tyr Ile Pro Ser His Leu Tyr Lys Ile
5          10          15          20

tca gga gga att atc atg ata agt gca ttt ggg ata ggt att gga act 1651
Ser Gly Gly Ile Ile Met Ile Ser Ala Phe Gly Ile Gly Ile Gly Thr
          25          30          35

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ctt att atc ttt tta atg atg att tcc ctt tta ttt att gga atg cca 1699  
 Leu Ile Ile Phe Leu Met Met Ile Ser Leu Leu Phe Ile Gly Met Pro  
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tta ggt ttt ctc act ggg tta atc gct tta gtt att tca tat ctt tgg 1747  
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 55 60 65

ttt gat act acc gca ata atg caa atg ata gct tca cgt gtc act gat 1795  
 Phe Asp Thr Thr Ala Ile Met Gln Met Ile Ala Ser Arg Val Thr Asp  
 70 75 80

ttc aca tca tct tac act ttt gta gct gtg cct atg ttt gtt ctt atg 1843  
 Phe Thr Ser Ser Tyr Thr Phe Val Ala Val Pro Met Phe Val Leu Met  
 85 90 95 100

gca aca tta ctt gat aag act gga att gct aga gat ctc tac aac gca 1891  
 Ala Thr Leu Leu Asp Lys Thr Gly Ile Ala Arg Asp Leu Tyr Asn Ala  
 105 110 115

atg cga gtc att ggc ggt cga tta cga ggt gga att gca att caa tgc 1939  
 Met Arg Val Ile Gly Gly Arg Leu Arg Gly Gly Ile Ala Ile Gln Ser  
 120 125 130

atg ttt gtt gca gtt cta ctt gct acg atg tca ggt att atc ggt gga 1987  
 Met Phe Val Ala Val Leu Leu Ala Thr Met Ser Gly Ile Ile Gly Gly  
 135 140 145

gaa act gtt tta tta ggc atg ttg gca tta cca caa atg tta cgc tta 2035  
 Glu Thr Val Leu Leu Gly Met Leu Ala Leu Pro Gln Met Leu Arg Leu  
 150 155 160

ggc tat aat aaa aac tta gct ata gga act gtt gta gca gga gga gca 2083  
 Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val Ala Gly Gly Ala  
 165 170 175 180

ttg ggt aca atg gtt cct cca agt atc gtg ttg att att tac gga atg 2131  
 Leu Gly Thr Met Val Pro Pro Ser Ile Val Leu Ile Ile Tyr Gly Met  
 185 190 195

acc gca aat gtt tct att gga gaa cta ttt ctt gca gca att cca gcc 2179  
 Thr Ala Asn Val Ser Ile Gly Glu Leu Phe Leu Ala Ala Ile Pro Ala  
 200 205 210

tcc tta cta ctt tct aca ttc tat att tta tat att cta gta ctt tgc 2227  
 Ser Leu Leu Leu Ser Thr Phe Tyr Ile Leu Tyr Ile Leu Val Leu Cys  
 215 220 225

tac ttc aaa cct agc tat ggc cct gca atg cct agc tca gaa aat cat 2275  
 Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Ser Ser Glu Asn His  
 230 235 240

aca tta acg aaa gaa gat att aaa aaa att att cat gat att gca att 2323  
 Thr Leu Thr Lys Glu Asp Ile Lys Lys Ile Ile His Asp Ile Ala Ile  
 245 250 255 260

cca gta gct atc gcc aca tgg att tta gga agt att tat ggc ggg ata 2371  
 Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile Tyr Gly Gly Ile  
 265 270 275

gca tca atc act gaa tct gcc tgt gtt ggt gta gtt ggg gta ata tta 2419  
 Ala Ser Ile Thr Glu Ser Ala Cys Val Gly Val Val Gly Val Ile Leu  
 280 285 290

gca gca ttc tat cga aaa gaa tta aat ttc aaa ata gta caa gaa tca 2467  
 Ala Ala Phe Tyr Arg Lys Glu Leu Asn Phe Lys Ile Val Gln Glu Ser  
 295 300 305  
 cta aaa cat aca atc aat act gtt ggt atg ata atc tgg gtc ggc att 2515  
 Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile Trp Val Gly Ile  
 310 315 320  
 ggc gca aca atg att ata ggt att tat aat cta atg ggt ggg gac cga 2563  
 Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met Gly Gly Asp Arg  
 325 330 335 340  
 ttt ata gct aac tta ttc gct agc tta gat gcc tct cca att tat act 2611  
 Phe Ile Ala Asn Leu Phe Ala Ser Leu Asp Ala Ser Pro Ile Tyr Thr  
 345 350 355  
 atc att att atg atg gtt att tta tta ata ctt ggt atg ttc tta gat 2659  
 Ile Ile Ile Met Met Val Ile Leu Leu Ile Leu Gly Met Phe Leu Asp  
 360 365 370  
 tgg att ggt gtt gcc atg ttg act ttc ctc aag aca agt aaa gcg aca 2707  
 Trp Ile Gly Val Ala Met Leu Thr Phe Leu Lys Thr Ser Lys Ala Thr  
 375 380 385  
 atc aat ttg tgt ttt gac ata gtc agg tac agt att tgg cgt ggt ccc 2755  
 Ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile Trp Arg Gly Pro  
 390 395 400  
 tcc ttc cac agt acc aat gtt cat cgt ggt acc ttt gtc ggg cgc ggt 2803  
 Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe Val Gly Arg Gly  
 405 410 415 420  
 act ttt tagtaaatct tgcgcgatac gaataaacgc attgatggca tttgctccgt 2859  
 Thr Phe  
 ttgtggatc gactgcgcga tgagcagatt tgccaaaaaa ttcaattaca tacttcccaa 2919  
 tcctttttct ttgcttaacg ttccactta gattgcccag aagccgatct gtctgaatgg 2979  
 gaacaagtgt tataccaaga agcgaatcca acaggtgaag tgggtgatcgg tatggtgggt 3039  
 aaatacactg aattaccgga tgcctacaaa tcgggttaatg aagccttgaa acaagcaggc 3099  
 ttaaaaaacc gtcttagcgt gcaaatcaaa tatattgatt cacaagatgt ggaaaccaa 3159  
 ggcacagaag tgtagaagg cgt 3182

&lt;210&gt; 73

&lt;211&gt; 422

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 73

Met Pro His His Cys Cys Ser Phe Ser Thr Thr Tyr Ile Pro Ser His  
 1 5 10 15  
 Leu Tyr Lys Ile Ser Gly Gly Ile Ile Met Ile Ser Ala Phe Gly Ile  
 20 25 30  
 Gly Ile Gly Thr Leu Ile Ile Phe Leu Met Met Ile Ser Leu Leu Phe  
 35 40 45

Ile Gly Met Pro Leu Gly Phe Leu Thr Gly Leu Ile Ala Leu Val Ile  
 50 55 60  
 Ser Tyr Leu Trp Phe Asp Thr Thr Ala Ile Met Gln Met Ile Ala Ser  
 65 70 75 80  
 Arg Val Thr Asp Phe Thr Ser Ser Tyr Thr Phe Val Ala Val Pro Met  
 85 90 95  
 Phe Val Leu Met Ala Thr Leu Leu Asp Lys Thr Gly Ile Ala Arg Asp  
 100 105 110  
 Leu Tyr Asn Ala Met Arg Val Ile Gly Gly Arg Leu Arg Gly Gly Ile  
 115 120 125  
 Ala Ile Gln Ser Met Phe Val Ala Val Leu Leu Ala Thr Met Ser Gly  
 130 135 140  
 Ile Ile Gly Gly Glu Thr Val Leu Leu Gly Met Leu Ala Leu Pro Gln  
 145 150 155 160  
 Met Leu Arg Leu Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val  
 165 170 175  
 Ala Gly Gly Ala Leu Gly Thr Met Val Pro Pro Ser Ile Val Leu Ile  
 180 185 190  
 Ile Tyr Gly Met Thr Ala Asn Val Ser Ile Gly Glu Leu Phe Leu Ala  
 195 200 205  
 Ala Ile Pro Ala Ser Leu Leu Leu Ser Thr Phe Tyr Ile Leu Tyr Ile  
 210 215 220  
 Leu Val Leu Cys Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Pro Ser  
 225 230 235 240  
 Ser Glu Asn His Thr Leu Thr Lys Glu Asp Ile Lys Lys Ile Ile His  
 245 250 255  
 Asp Ile Ala Ile Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile  
 260 265 270  
 Tyr Gly Gly Ile Ala Ser Ile Thr Glu Ser Ala Cys Val Gly Val Val  
 275 280 285  
 Gly Val Ile Leu Ala Ala Phe Tyr Arg Lys Glu Leu Asn Phe Lys Ile  
 290 295 300  
 Val Gln Glu Ser Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile  
 305 310 315 320  
 Trp Val Gly Ile Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met  
 325 330 335  
 Gly Gly Asp Arg Phe Ile Ala Asn Leu Phe Ala Ser Leu Asp Ala Ser  
 340 345 350  
 Pro Ile Tyr Thr Ile Ile Ile Met Met Val Ile Leu Leu Ile Leu Gly  
 355 360 365  
 Met Phe Leu Asp Trp Ile Gly Val Ala Met Leu Thr Phe Leu Lys Thr  
 370 375 380

Ser Lys Ala Thr ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile  
385 390 395 400

Trp Arg Gly Pro Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe  
405 410 415

Val Gly Arg Gly Thr Phe  
420

<210> 74  
<211> 2787  
<212> DNA  
<213> *Pasteurella multocida*

<220>  
<221> CDS  
<222> (463)..(936)

<220>  
<223> yhcJ

<400> 74  
gttaacacac catgattaat gatgccggtt gaagccactg caacgtaatc gaattgttcg 60  
gcatacaaa caagaatggt gccagtggtg tcatgcatcg cattggcagc atcagcttgt 120  
ggcgttgcaa tctgttgccg ttgttctatt ttgccgtctg ttacaatagc cgaggcaatt 180  
ttgtttccac caatatctaa tgctaaacag cgcataggct ctcttctgtg gatgacttat 240  
tttgcgatt tgacggcatc ggcaaacagg cttacgatat gttcgaggcg agtcagcgca 300  
gatcctacgg tgacagagta agcacaatc tcaattgcgg ttttcgccaa ttctgggggtg 360  
ttatagcgcc ctcttgccat cactcggcag ccagcagcat tcaaatcttt gactaaactga 420  
taatccggtt cagctggaat ttcaccgcca gtataaccag ac atg gtg cta cca 474  
Met Val Leu Pro  
1

ata att tct acc cct aag ttg tgg caa tac atc cct tct tca aaa tta 522  
Ile Ile Ser Thr Pro Lys Leu Trp Gln Tyr Ile Pro Ser Ser Lys Leu  
5 10 15 20

gaa caa tcc gcc atg gct aaa caa cct aat tct ttg att cgt tta ata 570  
Glu Gln Ser Ala Met Ala Lys Gln Pro Asn Ser Leu Ile Arg Leu Ile  
25 30 35

atg gct tca cgt gta gtt gga cgg acg cga tgg gta cca tca aaa gca 618  
Met Ala Ser Arg Val Val Gly Arg Thr Arg Ser Val Pro Ser Lys Ala  
40 45 50

ata ata tgg cgg cct gct cgg gct aac tct tca atg tct tgt aaa aat 666  
Ile Ile Ser Ala Pro Ala Ala Ala Asn Ser Ser Met Ser Cys Lys Asn  
55 60 65

ggg cta ata cga acg gga ctg tca ggt aaa tgg cgt tta acg ata cca 714  
Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg Leu Thr Ile Pro  
70 75 80

ata atc ggt aca ttg acg acg tta cgc gtg gct ttt aaa ttt tgg atc 762  
Ile Ile Gly Thr Leu Thr Thr Leu Arg Val Ala Phe Lys Phe Ser Ile

85	90	95	100			
cct tca ata cgt aac	ccg gca gca	cca ccg ata acg gat gct tgc gcc	810			
Pro Ser Ile Arg Asn	Pro Ala Ala	Pro Pro Ile Thr Asp Ala Cys Ala				
	105	110	115			
atg gcg gca aca att	tct ggc gag	tcc att ggc cca tta tct acg ggc	858			
Met Ala Ala Thr Ile	Ser Gly Glu	Ser Ile Gly Pro Leu Ser Thr Gly				
	120	125	130			
tgg caa gat gcg att aag cca tat	tta att tgt tct aaa act tgc gga	906				
Trp Gln Asp Ala Ile Lys	Pro Tyr Leu Ile Cys Ser Lys Thr Cys Gly					
	135	140	145			
tgt gat agt ttt gac ata tta act	cca gtc taaatttacc	aaaagaagat	956			
Cys Asp Ser Phe Asp Ile	Leu Thr Pro Val					
	150	155				
tgactccaat	ttgcataggt	taatcttaga	attaaaaaat	aacaacccaa	ataataaaaa	1016
tttgagatct	ttgtcgcata	tttattcata	gggaatagac	agcttaattt	tagttatgat	1076
ttgtcaatcc	ttgctatttt	ttgtgtttgc	tggtttcgca	tacactgttc	taattattgct	1136
ttgagcactt	gataaccttg	ctcattaaaa	tgtaatccgt	cggtacaaag	gcgtaaatcc	1196
agttcacctg	tagaatcaca	aaagtatttt	tggttttcaa	cgtaagtcac	gtctgacgga	1256
caatgttgtt	ttaaataggt	attgagcctg	tgaatttggt	cgttagtgtc	cgtaattaac	1316
tgattgaccg	gtgtggcttc	taataaaaaag	tagtgggacg	taggagaaat	ggtgtgtagg	1376
tgagtcagaa	tgctatttaa	ctatcgcatg	acttgccgcc	gtgaatacgt	ttcttcttta	1436
caaatatcat	tgacgcctaa	aaaaagaaaa	acagattgtc	caagttggtg	aatccgttta	1496
ggtttaacga	taacatccaa	atattgtcgc	gtactgacgc	cagaaagtcc	taaattggcg	1556
acggttttgt	ccgctaattg	agggtgtgct	gtacctgttt	cgccccacat	gtcaaaaagt	1616
gaatgaccaa	ttaagctgat	attggcaggt	ttggaaaatt	ccgccatttt	gctctgatag	1676
cgttgataaa	tatcctgatc	acttagcatg	tggtggacct	tattttgaaa	taaaacgcta	1736
agttatttat	aaaacctgat	atgcgcgtta	acagtaaaat	tatcttccgt	aggggttaaa	1796
attcaatttt	gtgacgaacc	tatcatttat	gaaataaaaac	ttcattttct	atataaaaaa	1856
tagttttttc	actttagaat	gccaaacgtg	tgaattttat	ttcatcatca	ttttaacgta	1916
atcccaacgt	aaaccaataga	ggagaactca	taatgaaatt	taaaaaacta	ctacttgcat	1976
ctttatgttt	agggtgttca	gcttctgtat	ttgcagcaga	ttacgatctt	aaattcggtg	2036
tggtgtcggg	tccaagctca	aacgaatata	aagcagtaga	attcttttgc	aaagaagtga	2096
aagaaaaaat	caatggcaaa	attgatgtgg	ctattttccc	tagctcacag	ttaggtgatg	2156
accgtgtgat	gattaaacaa	ttaaaagacg	gtgcattaga	ctttacgtta	ggtgaatcag	2216
cacgtttcca	aatttacttc	ccagaagcag	aagtatttgc	gttgccctat	atgattccta	2276
attttgaac	ctctaaaaaa	gcgttgctcg	acacaaaatt	tggtcaaggt	ttattgaaaa	2336

aaattgataa agagttaaac gtacaagtgt tatctgtggc gtataacggt acacgtcaaa 2396  
 caacttctaa ccgtgcaatc aacagcattg aagacatgaa aggggttaaaa ttacgtgtac 2456  
 ctaacgcggc aaccaacctt gcttatgcaa aatacgtggg tgcagcgcca acaccaatgg 2516  
 cattctctga agtttacctt gcgcttcaaa caaactctgt ggatgggtcaa gaaaacccat 2576  
 taccgacaat ccaagcacia aaattctatg aagtacaaaa atacttagcg ttaactaacc 2636  
 acatcttaaa tgaccaactt tacttaatca gtaacgatac gttggcagat ttaccagaag 2696  
 atttacaaaa agtgggttaa gatgcagcag cgaaagccgc tgaatatcac actaaactct 2756  
 tcgttgacgg tgagaacagc ttagtgtaat t 2787

<210> 75  
 <211> 158  
 <212> PRT  
 <213> Pasteurella multocida

<400> 75  
 Met Val Leu Pro Ile Ile Ser Thr Pro Lys Leu Trp Gln Tyr Ile Pro  
 1 5 10 15  
 Ser Ser Lys Leu Glu Gln Ser Ala Met Ala Lys Gln Pro Asn Ser Leu  
 20 25 30  
 Ile Arg Leu Ile Met Ala Ser Arg Val Val Gly Arg Thr Arg Ser Val  
 35 40 45  
 Pro Ser Lys Ala Ile Ile Ser Ala Pro Ala Ala Asn Ser Ser Met  
 50 55 60  
 Ser Cys Lys Asn Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg  
 65 70 75 80  
 Leu Thr Ile Pro Ile Ile Gly Thr Leu Thr Leu Arg Val Ala Phe  
 85 90 95  
 Lys Phe Ser Ile Pro Ser Ile Arg Asn Pro Ala Ala Pro Pro Ile Thr  
 100 105 110  
 Asp Ala Cys Ala Met Ala Ala Thr Ile Ser Gly Glu Ser Ile Gly Pro  
 115 120 125  
 Leu Ser Thr Gly Trp Gln Asp Ala Ile Lys Pro Tyr Leu Ile Cys Ser  
 130 135 140  
 Lys Thr Cys Gly Cys Asp Ser Phe Asp Ile Leu Thr Pro Val  
 145 150 155

<210> 76  
 <211> 2787  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <221> CDS  
 <222> (1949)..(2785)

&lt;220&gt;

&lt;223&gt; yiaO

&lt;400&gt; 76

gttaacacac catgattaat gatgccggtt gaagccactg caacgtaate gaattgtccg 60  
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 ggcgttgcaa tctgttggtg ttgtttctatt ttgcgctctg ttacaatagc cgaggcaatt 180  
 tttgttccac caatatctaa tgctaaacag cgcataggct ctcttctctg gatgacttat 240  
 tttgcgcatt tgacggcacc ggcaaacacg cttacgatat gttcagaggc agtcagcgca 300  
 gatcctacgg tgacagagta agcaccacac tcaattgcgg ttttcgccc tcttgggggtg 360  
 ttatagcgcc ctctcgccat cactcggcag ccagcagcat tcaaatcttt gactaaactga 420  
 taatccggtt cagctggaat ttcaccgcca gtataaccag acatggtgtc accaataatt 480  
 tctaccccca agttgtggca atacatccct tcttcaaaat tagaacaate cgccatggct 540  
 aaacaacctt attctttgat tctgttaata atggcttcac gtgtagtgtg acggacgcga 600  
 tccgttaccat caaaagcaat aatctcggcg cctgctgcgg ctaactcttc aatgtcttgt 660  
 aaaaatgggc taatacgaa cggactgtca ggtaaatcgc gtttaacgat accaataatc 720  
 ggtacattga cgcgtttacg cgtggctttt aaatttttga tcccttcaat acgtaaccgc 780  
 gcagcaccac cgataacgga tgcctgcgcc atggcggcaa caatttctcg cgagtcatt 840  
 ggccattat ctacgggctg gcaagatgcg attaagccat atttaatttg tcttaaaact 900  
 tgcggatgtg atagttttga catatttaact ccagtctaaa tttatcaaaa gaagattgac 960  
 tccaatttgc ataggttaat cttagaatta aaaaaataca accaaaaataa taaaaatttg 1020  
 agatctttgt cgcataatta ttcattagga atagacagct taatttttag tatgatttgt 1080  
 caatccctgc tattttttgt gtttgcgtgt ttgcgataca ctgttctaatt attgctttga 1140  
 gcacttgata accttgcctt ttaaaatgta atccgtcggc acaaaggcgt aaatccagtt 1200  
 caccgttaga atcacaaaag tattttttgt tttcaacgta agtcacgtct gacggacaat 1260  
 gttgttttaa ataggtattg agcctgtgaa tttgtgcgtt agtgaccgta ttaattctgat 1320  
 tgaccgggtg ggcttctaatt aaaaagtagt gggacgtagg agaaatgggt tgtagggtgag 1380  
 tcagaatgtc atttaactat cgcatactct gcgccgtgta atacgtttct tcttcaaaa 1440  
 tatcattgac gcttaaaaaa agaaaaacag attgtccaag ttgttgaaac cgttttaggtt 1500  
 taacgataac atccaaatat tgtcgcgtac tgacgccaga aagtcctaaa ttggcgacgg 1560  
 tttgtccgcg taattgaggt gtgcctgcta cctgttcgtc ccacatgtca aaaagtgaat 1620  
 gaccaattaa gctgatattg gcaggtttgg aaaattccgc cattttgctc tgatagcggt 1680  
 gataaatatc ctgatcaact agcatgtgtg gacctctatt ttgaaataaa acgctaagta 1740  
 ttatataaaa cctgatatgc cggtaaacag taaacttacc ttccgtaggg gtaaatattc 1800



aat gac caa ctt tac tta atc agt aac gat acg ttg gca gat tta cca 2692  
 Asn Asp Gln Leu Tyr Leu Ile Ser Asn Asp Thr Leu Ala Asp Leu Pro  
 235 240 245

gaa gat tta caa aaa gtg gtt aaa gat gca gca gcg aaa gcc gct gaa 2740  
 Glu Asp Leu Gln Lys Val Val Lys Asp Ala Ala Ala Lys Ala Ala Glu  
 250 255 260

tat cac act aaa ctc ttc gtt gac ggt gag aac agc tta gtt gaa tt 2787  
 Tyr His Thr Lys Leu Phe Val Asp Gly Glu Asn Ser Leu Val Glu  
 265 270 275

<210> 77

<211> 279

<212> PRT

<213> Pasteurella multocida

<400> 77

Met Lys Phe Lys Lys Leu Leu Leu Ala Ser Leu Cys Leu Gly Val Ser  
 1 5 10 15

Ala Ser Val Phe Ala Ala Asp Tyr Asp Leu Lys Phe Gly Met Val Ala  
 20 25 30

Gly Pro Ser Ser Asn Glu Tyr Lys Ala Val Glu Phe Phe Ala Lys Glu  
 35 40 45

Val Lys Glu Lys Ser Asn Gly Lys Ile Asp Val Ala Ile Phe Pro Ser  
 50 55 60

Ser Gln Leu Gly Asp Asp Arg Val Met Ile Lys Gln Leu Lys Asp Gly  
 65 70 75 80

Ala Leu Asp Phe Thr Leu Gly Glu Ser Ala Arg Phe Gln Ile Tyr Phe  
 85 90 95

Pro Glu Ala Glu Val Phe Ala Leu Pro Tyr Met Ile Pro Asn Phe Glu  
 100 105 110

Thr Ser Lys Lys Ala Leu Leu Asp Thr Lys Phe Gly Gln Gly Leu Leu  
 115 120 125

Lys Lys Ile Asp Lys Glu Leu Asn Val Gln Val Leu Ser Val Ala Tyr  
 130 135 140

Asn Gly Thr Arg Gln Thr Thr Ser Asn Arg Ala Ile Asn Ser Ile Glu  
 145 150 155 160

Asp Met Lys Gly Leu Lys Leu Arg Val Pro Asn Ala Ala Thr Asn Leu  
 165 170 175

Ala Tyr Ala Lys Tyr Val Gly Ala Ala Pro Thr Pro Met Ala Phe Ser  
 180 185 190

Glu Val Tyr Leu Ala Leu Gln Thr Asn Ser Val Asp Gly Gln Glu Asn  
 195 200 205

Pro Leu Pro Thr Ile Gln Ala Gln Lys Phe Tyr Glu Val Gln Lys Tyr  
 210 215 220

Leu Ala Leu Thr Asn His Ile Leu Asn Asp Gln Leu Tyr Leu Ile Ser  
 225 230 235 240

Asn Asp Thr Leu Ala Asp Leu Pro Glu Asp Leu Gln Lys Val Val Lys  
 245 250 255

Asp Ala Ala Ala Lys Ala Ala Glu Tyr His Thr Lys Leu Phe Val Asp  
 260 265 270

Gly Glu Asn Ser Leu Val Glu  
 275

<210> 78

<211> 2590

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (908) .. (1294)

<220>

<223> yjgF

<400> 78

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 aaagtgcggg ggcaattcgt tttattgagc aagtggacga gaaattgatt ttccgcagcg 180  
 gtggcgggat tacgatctta agcgagctag aagacgagta ccaagaattg atccaaaaag 240  
 tgtatgtacc agtaggataa gcgatgacat ttcctttatt tgagacgacg gctattgtga 300  
 acggtgaaat tcagcacctt gcctgcacgc aacaacgtta tgcggcaagt ttggcgacct 360  
 tttacggcga gaaaggagcg aaagtacagg atcttcgcaa aattattcag attccgacgc 420  
 cacttgaaca cactcaacat gcgccgataa tccgttgctg gattgattac aatcagcaag 480  
 actgtgacgt gcattatctt ccctatcaac gcaaaattta ccgcactttt cagcctgtca 540  
 tttgcgatga aattaactat gatctgaaat atgctgatcg ggcattatta aatcagttat 600  
 ttgctcagcg tagggattgt gatgagatta tgattatcaa acacggcaag gtgacggtat 660  
 gcagtatctg taatctggtg tttcgccaag gtgagcaatg gttcacgcca gatagccgct 720  
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 tctttattgca agagatcgca caattgaag aaattcggtt aattaatgca ctaaatcgcg 840  
 tgtaaatctt cttgaacag cgtaaaataa aacaactttt tcagtcagat aaaaggagat 900  
 aaacgac atg acg aaa gta att cat act gac aat gca cca gcc gcc att 949  
 Met Thr Lys Val Ile His Thr Asp Asn Ala Pro Ala Ala Ile  
 1 5 10  
 ggt cct tat gta caa gcg gta gat tta ggt aat atg ctg tta acc tct 997  
 Gly Pro Tyr Val Gln Ala Val Asp Leu Gly Asn Met Leu Leu Thr Ser  
 15 20 25 30  
 ggg caa att cca gtg aat cca aaa acc ggt gaa gtg cca gcg gat atc 1045  
 Gly Gln Ile Pro Val Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Ile

	35	40	45	
gta gca caa gca cgt caa tcg tta gaa aac gtg aaa gcg att gtg gaa				1093
Val Ala Gln Ala Arg Gln Ser Leu Glu Asn Val Lys Ala Ile Val Glu	50	55	60	
caa gcg gga tta caa gtc gca aat atc gtg aaa acc acg gtg ttt gtg				1141
Gln Ala Gly Leu Gln Val Ala Asn Ile Val Lys Thr Thr Val Phe Val	65	70	75	
aaa gat tta aat gac ttt gca g g gtc aat gcg gag tat gaa cgt ttc				1189
Lys Asp Leu Asn Asp Phe Ala Ala Val Asn Ala Glu Tyr Glu Arg Phe	80	85	90	
ttt aaa gag aac aat cac cct agc ttc cct gct cgt tca tgt gtg gaa				1237
Phe Lys Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu	95	100	105	110
gtg gca cgt ttg ccg aaa gat gtg ggg att gaa atc gag gca atc gct				1285
Val Ala Arg Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala	115	120	125	
gta aaa gcc taatgaatag cttgcattta tcttagtcgt agcaaaacaa				1334
Val Lys Ala				
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Arg Trp Lys Glu Leu Lys Lys His Lys Pro Gly Leu Val Ile Gly Val  
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Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro Met Ala Leu			
200	205	210	
gcg aaa ggc atg tta ggt aaa cat tac cgt tta ggt tgg gaa gag aaa 1087			
Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp Glu Glu Lys			
215	220	225	
gaa aaa gcc ggg cat tcc ctt gcg cca gaa ggc att att tct ctc ccg 1135			
Glu Lys Ala Gly His Ser Leu Ala Pro Glu Gly Ile Ile Ser Leu Pro			
230	235	240	
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Thr Arg Leu Pro Glu Ser Leu			
245	250		
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&lt;210&gt; 83

&lt;211&gt; 250

&lt;212&gt; PRT

<213> *Pasteurella multocida*

&lt;400&gt; 83

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 20 25 30  
 Leu Gln Gln Lys Gln Ser Leu Ala Arg Glu Gly Val Ala Leu Arg Pro  
 35 40 45  
 Pro Phe Ala Leu Glu Asn Glu Lys Ala Phe Ser Ala Ala Cys Ile Arg  
 50 55 60  
 Cys Gly Gln Cys Val Gln Ala Cys Pro His Glu Met Leu His Leu Ala  
 65 70 75 80  
 Ser Leu Ile Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg  
 85 90 95  
 Asp Lys Pro Cys Glu Met Cys Val Asp Ile Pro Cys Ala Lys Ala Cys  
 100 105 110  
 Pro Thr Gly Ala Leu Asp Asn Gln Ala Thr Glu Ile Asp Asp Ala Arg  
 115 120 125  
 Met Gly Leu Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln  
 130 135 140  
 Gly Leu Arg Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asn Lys  
 145 150 155 160  
 Ala Ile Thr Leu Val Met His Arg Asn Glu Arg Thr Gly Lys His Ala  
 165 170 175

Val Phe Ile Pro Thr Val His Ser Glu Ala Cys Thr Gly Cys Gly Lys  
 180 185 190

Cys Glu Glu Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro  
 195 200 205

Met Ala Leu Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp  
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Glu Glu Lys Glu Lys Ala Gly His Ser Leu Ala Pro Glu Gly Ile Ile  
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Ser Leu Pro Thr Arg Leu Pro Glu Ser Leu  
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<210> 84  
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 aaattgatcc gcgaagcgat tgagcaaggg ggtaagcgtg atattttaga ggatgtactg 360  
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 gaacaaaaca tcctcagaa aaaaacacgc aaaggcaag atcctcacgc gccttttgta 660  
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        1             5             10
ttg agt tat gtc gca tta atg gga ttc gcc ttt ccc att atg cgt tat 2497
Leu Ser Tyr Val Ala Leu Met Gly Phe Gly Phe Pro Ile Met Arg Tyr
      15             20             25
atg agt att cat ttt gat aca tta aat aat aac gct gtt cgc ttt etc 2545
Met Ser Ile His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu
      30             35             40             45
tca ggg ggc agc gtt ttt att tta gcc tgt ttt ttt tat tat cgc gct 2593
Ser Gly Gly Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala
      50             55             60
gag tta aca tct tcg ggg gct ggc gtc cag tcc gtt gcg atg ttg ccg 2641

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Glu Leu Thr Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro  
 65 70 75  
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 Ser Ser Ser Leu Gly Phe Leu Ile Leu Lys Thr Val Pro Ser Phe Ser  
 80 85 90  
 tac gtt aca atc tca aca ctt aat cgc gtt tgaccttcgc atttttgata 2739  
 Tyr Val Thr Ile Ser Thr Leu Asn Arg Val  
 95 100  
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&lt;210&gt; 85

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 85

Met Thr Lys Leu Ser Ile Gln Arg Asp Asn Leu Ile Cys Leu Ser Tyr  
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Val Ala Leu Met Gly Phe Gly Phe Pro Ile Met Arg Tyr Met Ser Ile  
 20 25 30

His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu Ser Gly Gly  
 35 40 45

Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala Glu Leu Thr  
 50 55 60

Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro Ser Ser Ser  
 65 70 75 80

Leu Gly Phe Leu Ile Leu Lys Thr Val Pro Ser Phe Ser Tyr Val Thr  
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Ile Ser Thr Leu Asn Arg Val

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<213> Artificial Sequence

<220>  
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19

<210> 87  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PRIMER

<400> 87  
cggccggtac cggcctagg

19

<210> 88  
<211> 18  
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<220>  
<223> Description of Artificial Sequence: primer

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18

<210> 89  
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<220>  
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<400> 89  
ctaggtaacct acaacctc

18

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<210> 91  
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<220>  
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<400> 91  
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<210> 92  
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taccctattct aaccaagc 18

<210> 93  
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<210> 95  
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<210> 96  
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<210> 97  
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 agataatgag ggtacattaa tcgatgaatt acaattagtg tataacaaag ctgcaccaagc 480  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 98  
 tctccattcc cttgtcgcgg caccc 25

<210> 99  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 99  
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<210> 100  
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 <212> DNA  
 <213> *Pasteurella multocida*

<220>  
 <223> cap5E

<220>  
 <221> CDS  
 <222> (1)..(1032)

<400> 100  
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 1 5 10 15

ggt aat gct gta ctc aaa cgt ttc tta gaa aca gat att cga gaa att 96  
 Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile  
 20 25 30

cgt gtt ttt tcg cgt gat gag aag aaa caa gat gac atg cgg aaa aaa 144  
 Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys  
 35 40 45

tat aat gat gca aaa tta aaa ttt tat att ggc gat gtt cgt gac tac 192  
 Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr  
 50 55 60

gat agt att tta aat gcc tcg cga ggt gtt gac tat att tat cat gct 240  
 Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala  
 65 70 75 80

gcc gca tta aag caa gtg cct tca tgc gag ttt tat cgg tta gag gca 288  
 Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala  
 85 90 95

gtg aaa acc aat att tta ggt acg gca aat gtc tta gaa gcc gcc atc 336  
 Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ala Ile  
 100 105 110

caa aac cag ata aaa cgc gtc gtc tgt ctt agc aca gat aaa gcg gtg 384  
 Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val  
 115 120 125

tac cca att aat gcg atg gcc att tct aaa gca atg atg gaa aaa gtc 432  
 Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val  
 130 135 140

atc atc gca aaa tcg cgt aac cta gaa ggc aca cca acg aca atc tgt 480  
 Ile Ile Ala Lys Ser Arg Asn Leu Glu Gly Thr Pro Thr Thr Ile Cys  
 145 150 155 160

tgt act cgc tat gcc aat gtc atg gca tcg cgt ggt tcg gtt atc cca 528  
 Cys Thr Arg Tyr Gly Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro  
 165 170 175

tta ttt gtc gat caa ata cgt caa ggc aag cct ttt act att act gat 576  
 Leu Phe Val Asp Gln Ile Arg Gln Gly Lys Pro Phe Thr Ile Thr Asp  
 180 185 190

cct gag atg aca cgc ttt atg atg aca ttg gaa gat gct gtg gat tta 624  
 Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu  
 195 200 205

gtc cta tat gca ttt aaa aat ggt caa aat ggt gat gtt ttt gta caa 672  
 Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln  
 210 215 220

aaa gcc ccc gca gca acc att ggt acc ctt gcc aaa gca att acc gaa 720  
 Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu  
 225 230 235 240

tta tta tct gtc cca aat cac cct att tcc att ata ggt acg cgt cat 768  
 Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His

	245	250	255	
gga gag aaa gca ttc gaa gct tta tta agc cgt gaa gaa atg gtt cat				816
Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His	260	265	270	
gca att aat gaa ggt aat tat tat cgc atc cca gcc gat caa cgc agt				864
Ala Ile Asn Glu Gly Asn Tyr Tyr Arg Ile Pro Ala Asp Gln Arg Ser	275	280	285	
tta aat tac agt aaa tat gtc gaa aaa ggg gaa cca aaa att acc gaa				912
Leu Asn Tyr Ser Lys Tyr Val Glu Lys Gly Pro Lys Ile Thr Glu	290	295	300	
gtc acc gac tac aac tca cat aat act gag cgt ttg act gtc aag gaa				960
Val Thr Asp Tyr Asn Ser His Asn Thr Glu Arg Leu Thr Val Lys Glu	305	310	315	320
atg aag cag tta ctg ctt aaa ctt gaa ttc ata cag aaa atg att gag				1008
Met Lys Gln Leu Leu Lys Leu Glu Phe Ile Gln Lys Met Ile Glu	325	330	335	
ggt gaa tac atc tca ccg gag gta ta				1034
Gly Glu Tyr Ile Ser Pro Glu Val	340			
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<211> 344				
<212> PRT				
<213> Pasteurella multocida				
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Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile	20	25	30	
Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys	35	40	45	
Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr	50	55	60	
Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala	65	70	75	80
Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala	85	90	95	
Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ala Ile	100	105	110	
Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val	115	120	125	
Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val	130	135	140	
Ile Ile Ala Lys Ser Arg Asn Leu Glu Gly Thr Pro Thr Thr Ile Cys	145	150	155	160

Cys Thr Arg Tyr Gly Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro  
 165 170 175  
 Leu Phe Val Asp Gln Ile Arg Gln Gly Lys Pro Phe Thr Ile Thr Asp  
 180 185 190  
 Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu  
 195 200 205  
 Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln  
 210 215 220  
 Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu  
 225 230 235 240  
 Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His  
 245 250 255  
 Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His  
 260 265 270  
 Ala Ile Asn Glu Gly Asn Tyr Tyr Arg Ile Pro Ala Asp Gln Arg Ser  
 275 280 285  
 Leu Asn Tyr Ser Lys Tyr Val Glu Lys Gly Glu Pro Lys Ile Thr Glu  
 290 295 300  
 Val Thr Asp Tyr Asn Ser His Asn Thr Glu Arg Leu Thr Val Lys Glu  
 305 310 315 320  
 Met Lys Gln Leu Leu Lys Leu Glu Phe Ile Gln Lys Met Ile Glu  
 325 330 335  
 Gly Glu Tyr Ile Ser Pro Glu Val  
 340

<210> 102  
 <211> 4931  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <223> fhaB2

<220>  
 <221> CDS  
 <222> (1)..(4929)

<220>  
 <221> misc\_feature  
 <222> 1632  
 <223> Xaa = any or unknown amino acid

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 1 5 10 15  
 ctc gtt cct gtg gca gaa tgt att aac tca gct att agc aat ggt tca 96  
 Leu Val Pro Val Ala Glu Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser

20	25	30	
tct gat tca aca tcc aca tca gaa caa gtt gaa gag gaa cct ttc ctt Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu 35 40 45			144
cta gaa caa tat tca ctt tcc tcc gtg tct tta tta gta aaa agc acg Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Val Lys Ser Thr 50 55 60			192
ttc aat cct gtt tcg tat gca atg caa ttg act tgg aaa cag ctt tct Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser 65 70 75 80			240
att tta ttt tta act gtg att tct gtt cct gtt ttg gct gag gga aaa Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys 85 90 95			288
ggg gat gaa aga aat caa tta aca gtg att gat aat agc gat cat att Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile 100 105 110			336
aaa tta gat gca tct aat ctt gct ggt aat gat aaa aca aaa atc tat Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr 115 120 125			384
caa gca gaa aat aaa gtt ctg gtt att gat att gct aaa cca aat ggg Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly 130 135 140			432
aaa ggg att tca gat aac cgt ttt gaa aaa ttt aat att cca aat agc Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser 145 150 155 160			480
gcg gtg ttt aat aat aat ggg act gaa gcg cag gca aga tca aca tta Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu 165 170 175			528
att ggt tac att ccg caa aat caa aat tta agg gga ggg aaa gaa gct Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala 180 185 190			576
gat gtt ata tta aat caa gtg aca ggt cct caa gaa agt aaa att gtt Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val 195 200 205			624
ggc gcg ctt gaa gta tta ggt aaa aaa gct gat atc gtc att gca aac Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn 210 215 220			672
caa aat ggt att acc tta aat ggt gta aga aca ata aat tca gat cgt Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg 225 230 235 240			720
ttt gtt gcc act acg agt gag ctt ata gat ccg aat cag atg atg tta Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu 245 250 255			768
aag gtt aca aaa gga aat gtg atc att gat att gat ggt ttt tcg aca Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr 260 265 270			816
gat gga tta aag tat tta gat att att gct aaa aaa att gaa caa aag			864

Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys	
275 280 285	
caa tca att aca tca ggg gat aat tca gaa gca aaa aca gat gtc act	912
Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr	
290 295 300	
ctt att gcg ggt tcc agt gaa tat gat tta agc aaa cat gag ctg aaa	960
Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys	
305 310 315	
aaa acg agc ggt gaa aat gta tct aat gat gtt att gct atc acg gga	1008
Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly	
325 330 335	
tct agt aca ggc gca atg cat ggt aaa aat att aag ttg att gtg aca	1056
Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr	
340 345 350	
gat aaa ggt gca ggc gta aaa cat gat gga att att ttg tct gaa aat	1104
Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn	
355 360 365	
gat att cag att gaa atg aat gaa ggt gac tta gaa ctt ggc aat acg	1152
Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr	
370 375 380	
att cag caa aca gtg gta aaa aaa gac cga aat att cga gcc aag aaa	1200
Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys	
385 390 395	
aaa att gaa gtg aaa aac gct aat cgt gtt ttt gtt ggt agt caa acg	1248
Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr	
405 410 415	
aaa tca gat gaa att tcg tta gag gcg aaa caa gtt aaa atc aga aaa	1296
Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys	
420 425 430	
aac gca gag att agg agt acg aca caa gcc aaa atc gta gca aag ggt	1344
Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly	
435 440 445	
gcc ctg tct att gag caa aat gcg aag ctc gtc gct aaa aag ata gat	1392
Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp	
450 455 460	
gtg gca aca gaa act cta act aat gct ggg cgt att tat ggt cga gag	1440
Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu	
465 470 475	
gtt aag ctt gac act aat aat ttg att aat gat aaa gaa att tat gct	1488
Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala	
485 490 495	
gaa cgg aaa ttg agt att ttg acg aaa gga aaa gat ctt gaa att att	1536
Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile	
500 505 510	
caa gat aga tat ttg tct cca ctg atg cgc gta aaa agt agt gtc cgc	1584
Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg	
515 520 525	

ttt tta ggc tct cgc ttt ttc tca ata tct cgc tcg atg ctc gca agc Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser 530 535 540	1632
ctt agt gca cag ttt aag cct ggt ttt gtg aat aag gga ctc att gaa Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu 545 550 555 560	1680
agt gcg ggg agt gca gaa tta act ttt aaa gaa aaa acc agt ttt tta Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu 565 570 575	1728
aca gag ggc aat aat ttt att aga gct aaa gat gcg tta act att aac Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn 580 585 590	1776
gcc caa aat att gaa att gat aaa aat caa gat att caa ttg ggt gct Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala 595 600 605	1824
aat ata acg ttg aat gtg gaa gaa aac ttt gtt aat cgt gca gga aca Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr 610 615 620	1872
ctg gca act ggt aaa aca ctg aca att aat acc gaa agt ggc agt att Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile 625 630 635 640	1920
tac aat ctt ggt ggg aca tta ggt gct gga aaa tca tta aaa ctg act Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr 645 650 655	1968
gct aaa tca acg gaa gaa ggt atg gga aat att gtt aac caa gaa aac Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn 660 665 670	2016
ggt tta ttc cat aca ctc ggt aat atg atg tta gaa gca gag cgt tct Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser 675 680 685	2064
gtt tat aat att ggc gat att tat gcg agt aaa aaa tta aca gtt cat Val Tyr Asn Ile Gly Asp Ile Tyr Thr Ala Ser Lys Lys Leu Thr Val His 690 695 700	2112
act cat aat ttg att aat gat gtg cgt tta tct ggc aat gtg agt tat Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr 705 710 715 720	2160
aag cct atc ggt tca agt cgt gat tat gat atc agt cgt gtt gcg gta Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val 725 730 735	2208
cat ggt tgg cac aat aat gtt tat aag ctc aac tta aat ctg caa gaa His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu 740 745 750	2256
caa gat aaa acc gat att aaa gtt gtg aaa atg ggg gct atc cgt tct Gln Asp Lys Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser 755 760 765	2304
gat ggt gat ttt gac ttt aag gga ata aag gcg aca tca tca gaa tca Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser 770 775 780	2352

aaa ccg cag tta att aat cat gga tta att aat gtc aaa gga aca ttt Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe 785 790 795 800	2400
aat gcg gaa gct gat caa gtg gtg aac caa atg aaa gcg ttt aac caa Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln 805 810 815	2448
aat gca tta gca agc gtg ttt aag aat cca gcg aaa atc acg atg tac Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr 820 825 830	2496
tat caa cca ctt act cgt tat att tgg aca cca tta tcg ggt aat gca Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala 835 840 845	2544
tcg cgt gaa ttt aac aat tta gag tct ttc ctc gat gcc ttg ttt ggc Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly 850 855 860	2592
tca aca aca atc tta aaa tca agt ttc tat agt acg gaa aat ttt agt Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser 865 870 875 880	2640
gct tat cag ctt cta tct cat att cag cat tca cca atg tac caa aaa Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys 885 890 895	2688
gcg atg gca caa gtg ttt ggt gca gag tgg cat agt aaa tcc tat gat Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp 900 905 910	2736
gag atg cga aac aaa tgg aaa agc ttt aaa gaa aat cca aca gat ttc Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe 915 920 925	2784
att tat tac cca tca gaa aaa gca aaa atc cta gcg gga aaa cta gaa Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu 930 935 940	2832
ggt aag ctt aca acg cta caa aat ggt gaa tat gcc gaa cgt ggt aag Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys 945 950 955 960	2880
ttt gat gag agt atc caa att ggt aaa cac caa tta tcg cta cca tca Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser 965 970 975	2928
gta gag ctt aaa gcg gag ttt agt gat aaa gaa cgt ttg gaa gag gac Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp 980 985 990	2976
ggg gta gat tta tcc tcg atc gcc gaa ctc tta gaa atg cca aac tta Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu 995 1000 1005	3024
ttt att gat aat agt atc caa tta gaa aag aaa aag ttg tct cct att Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile 1010 1015 1020	3072
gag gat cta gat gaa gaa cca cgt aaa aat ctg gat ata gaa gaa agc Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser 1025 1030 1035 1040	3120

cat tct aat tca tgc gat gac gtg ctt agc atg aat gat gat gag tct	3168
His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser	
1045 1050 1055	
gat aca gac gat agc aag tgg agt atg ggc aat gat gag aaa gag atg	3216
Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met	
1060 1065 1070	
ccc gat gat aag ctg ggt ata agt cgt gat gat cgt gga aat aaa cca	3264
Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro	
1075 1080 1085	
cct cgt act gat cct aca gtt gat tat ctt aac cct gat gaa ttc ttt	3312
Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe	
1090 1095 1100	
gaa aat ggt tat ctc ttg aat gag cta cta cag gag ctt gga gaa gag	3360
Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu	
1105 1110 1115 1120	
ccg tta cta aaa gaa ggg gaa gat cat ttt aaa cgt tct acc aat cta	3408
Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu	
1125 1130 1135	
gtc cgt cta ggc gag aga gat agg caa aat aga gaa aag aga gaa aaa	3456
Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys	
1140 1145 1150	
gag ggg tat ttt gat ctg cct ggt aca tta gat atg aaa ctg cag gag	3504
Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu	
1155 1160 1165	
tta ttc gaa aaa aga aaa caa aaa cac gaa gca gaa cag aaa gca aga	3552
Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg	
1170 1175 1180	
ata gaa aaa gca ctt cta caa aaa tca gaa caa caa gaa aaa cgt gtt	3600
Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Glu Gln Glu Lys Arg Val	
1185 1190 1195 1200	
gaa gaa cgt aag caa gag gaa aaa cgt caa gcg caa gat aaa att gct	3648
Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala	
1205 1210 1215	
aag caa gta gaa att gca aaa gaa atg caa cgg gta gaa gaa att cgc	3696
Lys Gln Val Glu Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg	
1220 1225 1230	
cag aga gaa aaa caa ctt gcg atc caa ctg caa gaa gaa gag aag aaa	3744
Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu Lys Lys	
1235 1240 1245	
caa caa gaa gaa aaa cat tta tcc gag gag aaa aaa caa gct gaa cag	3792
Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala Glu Gln	
1250 1255 1260	
aaa caa aaa gct gag gag aaa gtt gca caa gaa aga tta gac att gaa	3840
Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp Ile Glu	
1265 1270 1275 1280	
caa cag aaa gcg tat gaa gaa atg gcg aag cga gag gca gag gca tca	3888
Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser	
1285 1290 1295	

aaa aat gtt tta ttg aaa gcg att gat gaa gaa cgt cca aaa gtg gaa	3936
Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu	
1300 1305 1310	
act gat cca ctt ttc cgt aca aaa ttg aaa tat atc aat caa gat gac	3984
Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp	
1315 1320 1325	
tat gct ggt gca aat tat ttc ttc aat aaa gtt ggt tta aat aca aaa	4032
Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys	
1330 1335 1340	
ggt cat caa aaa gta aat gtg tta ggg gat aac tat ttt gat cat caa	4080
Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln	
1345 1350 1355 1360	
gtg att act cgc tcg att gag aaa aaa gta gat aac cac ctt aac caa	4128
Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln	
1365 1370 1375	
aaa tac aat ctc agc gat gtg gaa tta gtt aaa cag ctg atg gac aat	4176
Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn	
1380 1385 1390	
tcc aca aca caa gcg cag gag ttg gat ttg aaa cta ggt gcg gca tta	4224
Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Ala Ala Leu	
1395 1400 1405	
act aaa gaa caa caa gct aac ttg acc caa gat atc gtt tgg tat gtc	4272
Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val	
1410 1415 1420	
aaa acg aag gta aag ggc aaa gat gtg ttt gtt cca aag gtt tat ttc	4320
Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe	
1425 1430 1435 1440	
gct tct gaa acg ctc gta gaa gcc caa aaa tta caa ggt tta ggc act	4368
Ala Ser Glu Thr Leu Val Glu Ala Ala Gln Lys Leu Gln Gly Leu Gly Thr	
1445 1450 1455	
ggg act atc aga gtt ggt gaa gct aag att aaa gcc aaa gat gtg gtg	4416
Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val	
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aat acc ggg aca tta gct ggg aga aaa ctc aat gtt gaa gcg agt aat	4464
Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn	
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Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu	
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Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp	
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gaa tta gga gtc act gca caa cgc tca gaa atc aaa acg gaa ggt cat	4608
Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His	
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tta cat ctt gaa aca gat aag gat tca act att gat gta caa gca tcg	4656
Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser	
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gat att aaa gca aaa aca agc ttt gtg aag act ggt gat gtg aat ctc 4704
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Lys Asn  Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro
      1570                      1575                      1580

agt gca cta caa gtt gca gaa ctt gat gtg gca ggg ctt aaa gtc cca 4800
Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro
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ctt tta ggc gtg tcc gtc tcc atc cag ttt att cag agc ata cta gtg 4848
Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val
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agg caa ctt caa gag gga tca atc ttc gaa gta ggg cac tta cat ntt 4896
Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa
      1620                      1625                      1630

gcg gta gac aga aga tgt gaa cca agc ggg gag ta 4931
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&lt;210&gt; 103

&lt;211&gt; 1643

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 1632

&lt;223&gt; Xaa = any or unknown amino acid

&lt;400&gt; 103

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Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
      50          55          60

Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
      65          70          75          80

Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys
      85          90          95

Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile
      100          105          110

Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr
      115          120          125

Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly
      130          135          140

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Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser  
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 Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu  
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 Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala  
 180 185 190  
 Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val  
 195 200 205  
 Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn  
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 Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg  
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 Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu  
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 Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr  
 260 265 270  
 Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys  
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 Gln Ser Ile, Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr  
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 Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys  
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 Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr  
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 Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp  
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Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala  
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 Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile  
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 Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg  
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 Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser  
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 Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn  
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 Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser  
 675 680 685  
 Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His  
 690 695 700  
 Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr  
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 Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val  
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 His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu  
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 Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe  
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Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr  
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 Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala  
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 Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser  
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 Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu  
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 Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys  
                     945                    950                    955                    960  
 Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser  
                     965                    970                    975  
 Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp  
                     980                    985                    990  
 Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu  
                     995                    1000                    1005  
 Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile  
                     1010                    1015                    1020  
 Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser  
                     1025                    1030                    1035                    1040  
 His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser  
                     1045                    1050                    1055  
 Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met  
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 Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro  
                     1075                    1080                    1085  
 Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe  
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 Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu  
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 Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys  
                     1140                    1145                    1150

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 Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg  
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 Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys Arg Val  
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 Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu Lys Lys  
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 Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser  
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 Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln  
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 Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln  
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 Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn  
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 Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn  
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 pro gln ala glu ser thr ile ser thr ser ala arg tyr ser thr glu  
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 cgt cat aat ggt aat att aat aat att gaa tac gaa aat gtt agt tcg 144  
 arg his asn gly asn ile asn ile glu tyr glu asn val ser ser  
 35 40 45  
 ttg aaa gtt caa aaa ggg gca gct tct gta atg tat ggt agc ggt gcg 192  
 leu lys val gln lys gly ala ala ser val met tyr gly ser gly ala  
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 leu gly gly thr val glu phe thr thr lys asp ile glu asp phe val  
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100 105 110	
cac ttt ttt ggt ttt gta caa tta acc aaa cgt tgg ggg cat gaa aca His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr	384
115 120 125	
atc aac aac ggc aaa ggt aca gac att ctc ggc gaa cat cga ggt aaa Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys	432
130 135 140	
ccc aat ccg ctc aac tac tat act aca tca tgg tta acg aaa gtc ggt Pro Asn Pro Leu Asn Tyr Tyr Thr Thr Ser Trp Leu Thr Lys Val Gly	480
145 150 155	
tac gat att aat aac act cat cgt ttt aca ctg ttt tta gaa gat cgc Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg	528
165 170 175	
cgt gaa aag aag ctt acc gaa gaa aaa aca tta ggg ctt agt gat gca Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala	576
180 185 190	
gtg cgt ttt gct aat gat caa acc cct tat ctc cgt tat ggt att gaa Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu	624
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245 250 255	
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260 265 270	
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275 280 285	
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290 295 300	
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305 310 315	
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325 330 335	

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Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg	
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Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr	
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Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp	
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Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu	
565 570 575	
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&lt;210&gt; 105

&lt;211&gt; 669

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 105

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Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala  
 50 55 60

Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val  
 65 70 75 80

Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser  
 85 90 95

Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu  
 100 105 110

His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr  
 115 120 125

Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys  
 130 135 140

Pro Asn Pro Leu Asn Tyr Tyr Thr Thr Ser Trp Leu Thr Lys Val Gly  
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Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg  
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Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala  
 180 185 190

Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu  
 195 200 205  
 Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu  
 210 215 220  
 Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile  
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 Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser Phe Val Tyr Leu Gln  
 245 250 255  
 Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr Ser Pro Leu Tyr Trp  
 260 265 270  
 Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys  
 275 280 285  
 Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile  
 290 295 300  
 Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro  
 305 310 315 320  
 Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile  
 325 330 335  
 Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg Trp Asp His Tyr Asn  
 340 345 350  
 Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg  
 355 360 365  
 Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser Tyr Trp Gln Leu Ser Leu  
 370 375 380  
 Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr  
 385 390 395 400  
 Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly  
 405 410 415  
 Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr  
 420 425 430  
 Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His  
 435 440 445  
 Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu  
 450 455 460  
 Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr  
 465 470 475 480  
 Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu  
 485 490 495  
 Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala  
 500 505 510  
 Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser  
 515 520 525

Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp  
 530 535 540  
 Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser  
 545 550 555 560  
 Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu  
 565 570 575  
 Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu  
 580 585 590  
 Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser  
 595 600 605  
 Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp  
 610 615 620  
 Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr  
 625 630 635 640  
 Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala  
 645 650 655  
 Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe  
 660 665

&lt;210&gt; 106

&lt;211&gt; 908

&lt;212&gt; DNA

&lt;213&gt; Pasteurella multocida

&lt;220&gt;

&lt;223&gt; lgtC

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(906)

&lt;400&gt; 106

atg aat att tta ttt gtt tct gat gat gtt tat gct aaa cat ctg gtg 48  
 Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val  
 1 5 10 15

gtt gcg att aaa agc att ata aat cat aat gaa aaa ggt att tca ttt 96  
 Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe  
 20 25 30

tat att ttt gat ttg ggt ata aag gat gaa aat aag aga aat att aat 144  
 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn  
 35 40 45

gat att gtt tct tct tat gga agt gaa gtc aac ttt att gct gtg aat 192  
 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn  
 50 55 60

gag aaa gaa ttt gag agt ttt cct gtt caa att agt tat att tct tta 240  
 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu  
 65 70 75 80

gca aca tat gca agg cta aaa gcg gca gag tat ttg ccg gat aat tta	288
Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu	
85 90 95	
aat aaa att att tat tta gat gtt gat gtt ttg gtt ttt aac tca tta	336
Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu	
100 105 110	
gaa atg tta tgg aat gtt gat gtt aat aat ttt ctt acc gca gcc tgt	384
Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys	
115 120 125	
tat gat tct ttc atc gaa aat gaa aag tct gag cat aaa aaa tcg att	432
Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile	
130 135 140	
tca atg tca gat aag gaa tat tat ttt aat gca gga gta atg cta ttt	480
Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe	
145 150 155 160	
aat tta gat gaa tgg cgg aag atg gat gta ttc tca aga gct tta gac	528
Asn Leu Asp Glu Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile	
165 170 175	
ctg tta gct atg tat cct aat caa atg att tat cag gat caa gat ata	576
Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile	
180 185 190	
ttg aat atc ctt ttt agg aat aaa gtc tgt tat tta gat tgc aga ttt	624
Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe	
195 200 205	
aat ttc atg cca aat caa ctt gaa aga ata aaa caa tac cat aaa gga	672
Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly	
210 215 220	
aaa ttg agc aac tta cat tct tta gaa aaa aca acg atg cct gtc gtt	720
Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val	
225 230 235 240	
att tca cat tat tgt ggt cca gaa aaa gcg tgg cat gcg gat tgt aaa	768
Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys	
245 250 255	
cat ttt aat gta tat ttc tat cag aaa ata tta gca gaa ata acg aga	816
His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg	
260 265 270	
ggc acg gat aaa gaa cgc gta tta tct ata aaa act tat ctc aag gcc	864
Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala	
275 280 285	
ttg att aga agg att aga tat aaa ttc aaa tat caa gtc tat ta	908
Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr	
290 295 300	

&lt;210&gt; 107

&lt;211&gt; 302

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 107

Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val  
 1 5 10 15  
 Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe  
 20 25 30  
 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn  
 35 40 45  
 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn  
 50 55 60  
 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu  
 65 70 75 80  
 Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu  
 85 90 95  
 Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu  
 100 105 110  
 Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys  
 115 120 125  
 Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile  
 130 135 140  
 Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe  
 145 150 155 160  
 Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp  
 165 170 175  
 Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile  
 180 185 190  
 Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe  
 195 200 205  
 Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly  
 210 215 220  
 Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val  
 225 230 235 240  
 Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys  
 245 250 255  
 His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg  
 260 265 270  
 Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala  
 275 280 285  
 Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr  
 290 295 300

&lt;210&gt; 108

&lt;211&gt; 2054

&lt;212&gt; DNA

&lt;213&gt; Pasteurella multocida

&lt;220&gt;

&lt;223&gt; pnp

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (2052)

&lt;400&gt; 108

atg	gca	agt	atg	gat	gat	act	act	gtg	ttt	gtc	aca	gtg	gtt	gcc	aaa	48
Met	Ala	Ser	Met	Asp	Asp	Thr	Thr	Val	Phe	Val	Thr	Val	Val	Ala	Lys	
	1				5				10					15		

aaa	gat	gtg	aaa	gaa	ggg	caa	gac	ttc	ttc	cca	tta	act	gtt	aac	tat	96
Lys	Asp	Val	Lys	Glu	Gly	Gln	Asp	Phe	Phe	Pro	Leu	Thr	Val	Asn	Tyr	
		20						25					30			

caa	gag	cgt	act	tat	gct	gca	ggc	cgt	att	cct	ggg	ggc	ttt	ttc	aaa	144
Gln	Glu	Arg	Thr	Tyr	Ala	Ala	Gly	Arg	Ile	Pro	Gly	Gly	Phe	Phe	Lys	
		35					40					45				

cgt	gaa	ggg	cgt	cct	tct	gaa	ggc	gaa	act	tta	att	gct	cgt	tta	att	192
Arg	Glu	Gly	Arg	Pro	Ser	Glu	Gly	Glu	Thr	Leu	Ile	Ala	Arg	Leu	Ile	
	50					55					60					

gac	cgt	cca	att	cgt	cct	ctt	ttc	cca	gaa	ggg	ttt	tat	aac	gaa	atc	240
Asp	Arg	Pro	Ile	Arg	Pro	Leu	Phe	Pro	Glu	Gly	Phe	Tyr	Asn	Glu	Ile	
	65				70					75				80		

caa	atc	gtg	gcg	aca	gtg	gtg	tct	gtt	aat	ccg	caa	att	tgt	cca	gat	288
Gln	Ile	Val	Ala	Met	Ile	Val	Val	Ser	Val	Asn	Pro	Gln	Ile	Cys	Pro	
			85						90					95		

tta	gtg	gca	atg	atc	ggg	gca	tct	gcg	gca	ctt	tct	tta	tca	ggg	gtg	336
Leu	Val	Ala	Met	Ile	Gly	Ala	Ser	Ala	Ala	Leu	Ser	Leu	Ser	Gly	Val	
		100						105					110			

cca	ttt	aat	ggc	cct	atc	ggg	gcg	gca	cgt	gtt	ggg	ttt	att	gat	gat	384
Pro	Phe	Asn	Gly	Pro	Ile	Gly	Ala	Ala	Arg	Val	Gly	Phe	Ile	Asp	Asp	
		115					120					125				

caa	ttt	gtg	tta	aac	cca	acc	atg	aac	gag	caa	aaa	caa	agc	cgt	tta	432
Gln	Phe	Val	Leu	Asn	Pro	Thr	Met	Asn	Glu	Gln	Lys	Gln	Ser	Arg	Leu	
		130				135					140					

gac	ttg	gtt	gtc	gcg	gga	aca	gat	aaa	gcg	gtg	tta	atg	gtg	gaa	tct	480
Asp	Leu	Val	Val	Ala	Gly	Thr	Asp	Lys	Ala	Val	Leu	Met	Val	Glu	Ser	
	145				150				155					160		

gaa	gcc	gat	gta	tta	acc	gaa	gaa	caa	atg	tta	gct	gcg	gtg	gtg	ttt	528
Glu	Ala	Asp	Val	Leu	Thr	Glu	Glu	Gln	Met	Leu	Ala	Ala	Val	Val	Phe	
			165						170					175		

ggg	cat	cag	caa	caa	caa	gtg	gtg	att	gac	gcg	atc	aaa	gaa	ttt	acc	576
Gly	His	Gln	Gln	Gln	Gln	Val	Val	Ile	Asp	Ala	Ile	Lys	Glu	Phe	Thr	
		180						185					190			

gca	gaa	gcc	ggg	aaa	ccg	cgt	tgg	gat	tgg	gtg	gca	cct	gaa	cca	aat	624
Ala	Glu	Ala	Gly	Lys	Pro	Arg	Trp	Asp	Trp	Val	Ala	Pro	Glu	Pro	Asn	
		195				200						205				

acc	gcg	tta	att	gaa	aaa	gtg	aaa	gcg	att	gca	gaa	gcg	cgt	tta	ggc	672
Thr	Ala	Leu	Ile	Glu	Lys	Val	Lys	Ala	Ile	Ala	Glu	Ala	Arg	Leu	Gly	
		210				215						220				

gaa gca tac cgt atc act gaa aaa caa gca cgt tat gaa caa att gat Glu Ala Tyr Arg Ile Thr Glu Lys Gln Ala Arg Tyr Glu Gln Ile Asp 225 230 235	720
gcg att aaa gct gat gtg att gca caa atc aca gct gaa gta gca gaa Ala Ile Lys Ala Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu 245 250 255	768
ggc gaa gac atc agt gaa ggg aaa att gtc gat att ttc acc gca ctt Gly Glu Asp Ile Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu 260 265 270	816
gaa agc caa atc gta cgt agc cgt atc att gct ggt gaa cca cgt att Glu Ser Gln Ile Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile 275 280 285	864
gat ggt cgt aca gtg gat act gtt cgt gca tta gat att tgt act ggt Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly 290 295 300	912
gtt tta cca cgt aca cac ggt tct gcg att ttc acc cgt ggt gaa aca Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr 305 310 315 320	960
cag gcg tta gct gtc gcg aca tta ggt aca gaa cgt gat gca caa att Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile 325 330 335	1008
att gat gaa tta aca ggt gag cgt tca gat cac ttc tta ttc cac tac Ile Asp Glu Leu Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr 340 345 350	1056
aac ttc ccg cca tat tct gtg ggt gaa acc ggt atg att ggt tca cca Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro 355 360 365	1104
aaa cgt cgt gaa att ggt cat ggt cgt tta gcg aaa cgc ggt gta gct Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala 370 375 380	1152
gca gtg atg cca aca ctt gcc gag ttc ccg tat gtg gta cgt gtt gtc Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val 385 390 395 400	1200
tct gaa atc aca gaa tca aat ggt tct tct tct atg gca tgc gtt tgt Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Met Ala Ser Val Cys 405 410 415	1248
ggt gcg tct tta gca tta atg gat gcg ggt gta cca att aaa gcg gcg Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala 420 425 430	1296
gtt gca ggt att gca atg gcc tta gtc aaa gaa gac gaa aaa ttt gtg Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val 435 440 445	1344
gtg ctt tca gac atc tta ggt gat gaa gat cac tta ggt gac atg gac Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp 450 455 460	1392
ttc aaa gtc gcg ggt aca cgt acg ggt gtg acg gca tta caa atg gat Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp 465 470 475 480	1440

atc aaa atc gaa ggt atc aca gca gaa atc atg caa att gcg tta aac 1488  
 Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn  
 485 490 495

caa gcg aaa agc gca cgt tta cac att tta ggt gtg atg gag caa gcg 1536  
 Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala  
 500 505 510

atc cca gcg cca cgt gcg gat att tct gat ttt gca ccg cgt att tac 1584  
 Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr  
 515 520 525

act atg aaa att gat ccg aag aaa atc aaa gat gtg atc ggt aaa ggt 1632  
 Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly  
 530 535 540

ggt gca acc att cgt gcc tta aca gaa gaa aca ggt acc tca att gat 1680  
 Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp  
 545 550 555 560

atc gat gat gat ggt acg gtg aag att gct gcg gtt gat ggc aat tca 1728  
 Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser  
 565 570 575

gca aaa gag gtg atg gcg cgt att gaa gat att act gca gaa gtt gaa 1776  
 Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu  
 580 585 590

gcg ggt gca gtg tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt 1824  
 Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly  
 595 600 605

gcc ttc gtt tct atc gta ggt aac aaa gaa ggc tta gtg cat att tct 1872  
 Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser  
 610 615 620

caa atc gcg gaa gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg 1920  
 Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val  
 625 630 635 640

ggg caa gaa gtg act gtt aaa gtg gtt gag att gat cgt caa ggt cgt 1968  
 Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg  
 645 650 655

att cgt tta acc atg aaa gaa gtt gca cca aag caa gaa cac gtt gat 2016  
 Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp  
 660 665 670

tct gtt gtc gca gac gtt gcc gca gaa gaa aac gca ta 2054  
 Ser Val Val Ala Asp Val Ala Ala Glu Glu Asn Ala  
 675 680

&lt;210&gt; 109

&lt;211&gt; 684

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 109

Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys  
 1 5 10 15

Lys Asp Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asn Tyr

20					25					30					
Gln	Glu	Arg	Thr	Tyr	Ala	Ala	Gly	Arg	Ile	Pro	Gly	Gly	Phe	Phe	Lys
		35					40					45			
Arg	Glu	Gly	Arg	Pro	Ser	Glu	Gly	Glu	Thr	Leu	Ile	Ala	Arg	Leu	Ile
	50					55					60				
Asp	Arg	Pro	Ile	Arg	Pro	Leu	Phe	Pro	Glu	Gly	Phe	Tyr	Asn	Glu	Ile
65					70					75				80	
Gln	Ile	Val	Ala	Thr	Val	Val	Ser	Val	Asn	Pro	Gln	Ile	Cys	Pro	Asp
			85						90					95	
Leu	Val	Ala	Met	Ile	Gly	Ala	Ser	Ala	Ala	Leu	Ser	Leu	Ser	Gly	Val
		100						105					110		
Pro	Phe	Asn	Gly	Pro	Ile	Gly	Ala	Ala	Arg	Val	Gly	Phe	Ile	Asp	Asp
		115					120					125			
Gln	Phe	Val	Leu	Asn	Pro	Thr	Met	Asn	Glu	Gln	Lys	Gln	Ser	Arg	Leu
	130						135					140			
Asp	Leu	Val	Val	Ala	Gly	Thr	Asp	Lys	Ala	Val	Leu	Met	Val	Glu	Ser
145						150					155			160	
Glu	Ala	Asp	Val	Leu	Thr	Glu	Glu	Gln	Met	Leu	Ala	Ala	Val	Val	Phe
			165					170						175	
Gly	His	Gln	Gln	Gln	Gln	Val	Val	Ile	Asp	Ala	Ile	Lys	Glu	Phe	Thr
		180						185					190		
Ala	Glu	Ala	Gly	Lys	Pro	Arg	Trp	Asp	Trp	Val	Ala	Pro	Glu	Pro	Asn
		195					200					205			
Thr	Ala	Leu	Ile	Glu	Lys	Val	Lys	Ala	Ile	Ala	Glu	Ala	Arg	Leu	Gly
	210					215					220				
Glu	Ala	Tyr	Arg	Ile	Thr	Glu	Lys	Gln	Ala	Arg	Tyr	Glu	Gln	Ile	Asp
225						230					235			240	
Ala	Ile	Lys	Ala	Asp	Val	Ile	Ala	Gln	Ile	Thr	Ala	Glu	Val	Ala	Glu
			245					250						255	
Gly	Glu	Asp	Ile	Ser	Glu	Gly	Lys	Ile	Val	Asp	Ile	Phe	Thr	Ala	Leu
	260							265					270		
Glu	Ser	Gln	Ile	Val	Arg	Ser	Arg	Ile	Ile	Ala	Gly	Glu	Pro	Arg	Ile
	275						280					285			
Asp	Gly	Arg	Thr	Val	Asp	Thr	Val	Arg	Ala	Leu	Asp	Ile	Cys	Thr	Gly
	290					295					300				
Val	Leu	Pro	Arg	Thr	His	Gly	Ser	Ala	Ile	Phe	Thr	Arg	Gly	Glu	Thr
	305					310					315			320	
Gln	Ala	Leu	Ala	Val	Ala	Thr	Leu	Gly	Thr	Glu	Arg	Asp	Ala	Gln	Ile
			325					330						335	
Ile	Asp	Glu	Leu	Thr	Gly	Glu	Arg	Ser	Asp	His	Phe	Leu	Phe	His	Tyr
	340						345					350			
Asn	Phe	Pro	Pro	Tyr	Ser	Val	Gly	Glu	Thr	Gly	Met	Ile	Gly	Ser	Pro

355		360		365
Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala				
370		375		380
Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val				
385		390		400
Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Met Ala Ser Val Cys				
	405		410	415
Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala				
	420		425	430
Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val				
	435		440	445
Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp				
	450		455	460
Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp				
465		470		475
Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn				
	485		490	495
Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala				
	500		505	510
Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr				
	515		520	525
Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly				
	530		535	540
Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp				
545		550		555
Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser				
	565		570	575
Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu				
	580		585	590
Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly				
	595		600	605
Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser				
	610		615	620
Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val				
	625		630	635
Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg				
	645		650	655
Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp				
	660		665	670
Ser Val Val Ala Asp Val Ala Ala Glu Glu Asn Ala				
	675		680	

<210> 110  
 <211> 1514  
 <212> DNA  
 <213> *Pasteurella multocida*

<220>  
 <223> purF

<220>  
 <221> CDS  
 <222> (1)..(1512)

<400> 110  
 atg tgt ggt att gtt ggt att gtt agc caa agc ccc gtt aac caa tca 48  
 Met Cys Gly Ile Val Gly Ile Val Ser Gln Ser Pro Val Asn Gln Ser  
 1 5 10 15  
 att tat gat gcg tta acc tta ttg caa cac cgc ggg caa gac gcc gcc 96  
 Ile Tyr Asp Ala Leu Thr Leu Leu His Arg Gly Gln Asp Ala Ala  
 20 25 30  
 ggg att gta acc gta gat gat gaa aac cga ttc cgc ttg cgt aaa gcg 144  
 Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala  
 35 40 45  
 aac ggg tta gtc agc gat gta ttt gaa caa gtt cat atg tta cgt tta 192  
 Asn Gly Leu Val Ser Asp Val Phe Glu Gln Val His Met Leu Arg Leu  
 50 55 60  
 caa ggc aat gct ggc att gga cat gtt cgt tat cct acg gct ggg agc 240  
 Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser  
 65 70 75 80  
 tca agt gtc tct gaa gcg caa cct ttt tat gta aat tcg cct tat ggc 288  
 Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly  
 85 90 95  
 tta acc tta gtg cat aat ggt aac ttg acc aat tca agt gaa tta aaa 336  
 Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys  
 100 105 110  
 gaa aag tta ttt cgt ctc gca cgt cgc cat gta aat acc aat tca gat 384  
 Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp  
 115 120 125  
 tct gaa tta tta ctc aat atc tta gcc aat cac ctt gat cac ttc gaa 432  
 Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu  
 130 135 140  
 aaa tac caa tta gat ccg caa gat gta ttc agt gct gtc aaa caa acg 480  
 Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr  
 145 150 155 160  
 cat cag gat att cgt ggt gct tat gct tgt atc gcc atg att att ggt 528  
 His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly  
 165 170 175  
 cat ggt atg gtc gcg ttt cgt gat ccg aac ggt atc cgt ccg tta gtg 576  
 His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val  
 180 185 190  
 tta ggg aaa cgc gag gaa aat ggc aaa aca gag tat atg ttt gcc tcc 624  
 Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser

195	200	205	
gaa agt atc gca tta gat aca gtg ggt ttt gag ttt gta cga gat gta Glu Ser Ile Ala Leu Asp Thr Val Gly Phe Glu Phe Val Arg Asp Val 210 215 220			672
caa ccc ggc gaa gcg att tat gtc acg ttt gaa ggg gaa atg tat gct Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala 225 230 235 240			720
cag caa tgc gca gac aaa cca aca tta aca cct tgt att ttt gaa tac Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr 245 250 255			768
gtc tat ttt gca cgt cca gac tct tgc atc gat ggg gtt tct gtt tat Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr 260 265 270			816
gct gcc cgt gtt cat atg gga caa cgt tta ggt gaa aaa att gca cgg Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg 275 280 285			864
gaa tgg gcg gat gtg gat gat att gat gtg gtc att cct gtg cct gaa Glu Trp Ala Asp Val Asp Asp Ile Asp Val Val Ile Pro Val Pro Glu 290 295 300			912
acc tct aac gat att gct tta cgt att gcg cgc gtg tta aat aaa cgc Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro 305 310 315 320			960
tat cgt caa ggt ttt gtg aaa aat cgc tat gta gga cgt acg ttt att Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile 325 330 335			1008
atg ccg ggg cag gca ttg cga gtc agt tct gtt aga cgt aaa ctc aat Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn 340 345 350			1056
acc att gct tca gaa ttt aaa gat aag aat gtg tta tta gtt gac gac Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp 355 360 365			1104
tcg att gta cgt ggt acc acg tct gaa caa att gtc gaa atg gcg aga Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg 370 375 380			1152
gcg gca ggt gcg aag aaa att tat ttt gcc tct gct gca cca gaa att Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile 385 390 395 400			1200
cgt tat cca aat gtg tat ggt att gat atg cca acc aaa aat gaa ttg Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu 405 410 415			1248
atc gct tat ggt cgt gat gta gat gaa att gct aac tta att ggt gtg Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val 420 425 430			1296
gat aaa ttg att ttc caa gat ttg gat gcg tta act ggt tct gtg caa Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln 435 440 445			1344
caa gaa aat cca agt att caa gac ttt gat tgt tcg gtg ttt aca ggg			1392

Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly  
 450 455 460  
 gtt tat gtg acg ggc gat att aca cct gaa tat ctg gat aat att gca 1440  
 Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala  
 465 470 475 480  
 gaa cag cgt aat gat atc gcc aag aaa aag cgt gaa aaa gat gct acc 1488  
 Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr  
 485 490 495  
 aat ctt gaa atg cac aat gaa aaa ta 1514  
 Asn Leu Glu Met His Asn Glu Lys  
 500  
  
 <210> 111  
 <211> 504  
 <212> PRT  
 <213> *Pasteurella multocida*  
  
 <400> 111  
 Met Cys Gly Ile Val Gly Ile Val Ser Gln Ser Pro Val Asn Gln Ser  
 1 5 10 15  
 Ile Tyr Asp Ala Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala  
 20 25 30  
 Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala  
 35 40 45  
 Asn Gly Leu Val Ser Asp Val Phe Glu Gln Val His Met Leu Arg Leu  
 50 55 60  
 Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser  
 65 70 75 80  
 Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly  
 85 90 95  
 Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys  
 100 105 110  
 Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp  
 115 120 125  
 Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu  
 130 135 140  
 Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr  
 145 150 155 160  
 His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly  
 165 170 175  
 His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val  
 180 185 190  
 Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser  
 195 200 205  
 Glu Ser Ile Ala Leu Asp Thr Val Gly Phe Glu Phe Val Arg Asp Val  
 210 215 220

Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala  
 225 230 235 240  
 Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr  
 245 250 255  
 Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr  
 260 265 270  
 Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg  
 275 280 285  
 Glu Trp Ala Asp Val Asp Asp Ile Asp Val Val Ile Pro Val Pro Glu  
 290 295 300  
 Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro  
 305 310 315 320  
 Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile  
 325 330 335  
 Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn  
 340 345 350  
 Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp  
 355 360 365  
 Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg  
 370 375 380  
 Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile  
 385 390 395 400  
 Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu  
 405 410 415  
 Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val  
 420 425 430  
 Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln  
 435 440 445  
 Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly  
 450 455 460  
 Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala  
 465 470 475 480  
 Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr  
 485 490 495  
 Asn Leu Glu Met His Asn Glu Lys  
 500

<210> 112  
 <211> 989  
 <212> DNA  
 <213> *Pasteurella multocida*  
 <220>  
 <223> rci

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(987)

&lt;400&gt; 112

atg gca aca ata aga aaa cgt ggt aac tca tat cgt gct gag ata agc	48
Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser	
1 5 10 15	
aaa aac gga gta agg aaa tca gca aca ttt aag act aaa tca gaa gct	96
Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala	
20 25 30	
aat gcg tgg gct gtt gac gag gag aga aaa tta gct gat ttg gca aaa	144
Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys	
35 40 45	
ggt atc gct cca gat att att ttt aga gat gta ata gaa cgc tat caa	192
Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln	
50 55 60	
aat gaa gtg tct ata act aaa aaa ggc gcg cga aat gaa att ata aga	240
Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg	
65 70 75 80	
tta aac cgc ttt tta aga tat gat att tct aat ctg tat att cgt gat	288
Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp	
85 90 95	
tta aga aaa gaa gat ttt gag gag tgg atc aga att cgc cta acc gaa	336
Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu	
100 105 110	
gta tcg gat gct agc gtt aga cgt gag ctt gtt act ata tcg tca gtg	384
Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val	
115 120 125	
ctg aca aca gca ata aat aag tgg gga tat att tca agg cat cca atg	432
Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met	
130 135 140	
act ggt att gaa aaa cca aaa aac tcg gca gaa aga aaa gaa cga tat	480
Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr	
145 150 155 160	
tca gaa cag gac att aaa aca ata tta gaa aca gct aga tat tgt gaa	528
Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu	
165 170 175	
gat aaa cta ccc ata aca ctc aaa caa aga gta gca att gca atg tta	576
Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu	
180 185 190	
ttt gct att gaa acc gct atg cgt gct ggt gag att gct agt ata aaa	624
Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys	
195 200 205	
tgg gat aat gtt ttt ctt gaa aag aga ata gta cat tta ccg aca act	672
Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr	
210 215 220	

aaa aac ggg cac tct aga gat gtg ccg ctt tgc caa aga gct gtt gcg 720  
 Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala  
 225 230 235 240  
 cta att tta aaa atg aaa gag gta gaa aat gga gat ctt gtg ttt cag 768  
 Leu Ile Leu Lys Met Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln  
 245 250 255  
 acc acg cct gaa tca tta agc acc acg ttt aga gtg tta aag aaa gag 816  
 Thr Thr Pro Glu Ser Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu  
 260 265 270  
 tgt gga ctt gaa cat ctc cat ttt cat gat acg aga agg gaa gcg ttg 864  
 Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu  
 275 280 285  
 acg aga tta tct aag aaa gta gat gta atg act cta gcc aaa att agc 912  
 Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser  
 290 295 300  
 gga cat aga gat tta aga att tta caa aac aca tat tac gca ccg aat 960  
 Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn  
 305 310 315 320  
 atg agt gaa gtg gca aac ttg ttg gat ta 989  
 Met Ser Glu Val Ala Asn Leu Leu Asp  
 325

&lt;210&gt; 113

&lt;211&gt; 329

&lt;212&gt; PRT

<213> *Pasteurella multocida*

&lt;400&gt; 113

Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser  
 1 5 10 15  
 Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala  
 20 25 30  
 Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys  
 35 40 45  
 Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln  
 50 55 60  
 Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg  
 65 70 75 80  
 Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp  
 85 90 95  
 Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu  
 100 105 110  
 Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val  
 115 120 125  
 Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met  
 130 135 140  
 Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr

145                      150                      155                      160  
 Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu  
                                  165                                   170                                   175  
 Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu  
                                  180                                   185                                   190  
 Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys  
                                  195                                   200                                   205  
 Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr  
                                  210                                   215                                   220  
 Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala  
                                  225                                   230                                   235                                   240  
 Leu Ile Leu Lys Met Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln  
                                  245                                   250                                   255  
 Thr Thr Pro Glu Ser Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu  
                                  260                                   265                                   270  
 Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu  
                                  275                                   280                                   285  
 Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser  
                                  290                                   295                                   300  
 Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn  
                                  305                                   310                                   315                                   320  
 Met Ser Glu Val Ala Asn Leu Leu Asp  
                                  325

&lt;210&gt; 114

&lt;211&gt; 1190

&lt;212&gt; DNA

<213> *Pasteurella multocida*

&lt;220&gt;

&lt;223&gt; sopE

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1188)

&lt;400&gt; 114

atg tct gaa gaa tat cta cat ggt gtc aaa gtc aca gaa atc aat caa 48  
 Met Ser Glu Glu Tyr Leu His Gly Val Lys Val Thr Glu Ile Asn Gln  
                                  1                                   5                                   10                                   15

gca att cgc aca att caa agt cta tca acc gca gtc atc ggt att gtc 96  
 Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val  
                                  20                                   25                                   30

tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat att gtc 144  
 Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro  
                                  35                                   40                                   45

gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga aaa caa 192  
 Val Leu Ile Thr Asn Val Ala Ala Ile Gly Lys Ala Gly Lys Gln

50	55	60	
ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc aat tgc 240 Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys 80 65 70 75			
aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac gaa gaa 288 Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu 95 85 90			
aca aaa gca agt gaa atg aac acg gca att att gcg aca atc aca gaa 336 Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu 110 100 105			
gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa aac aaa 384 Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys 125 115 120			
ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac aca aaa 432 Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys 140 130 135			
gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac gca ttt 480 Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe 155 145 150			
gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg gtg caa 528 Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln 170 165 175			
tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg ggc gat 576 Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp 190 180 185			
ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac tat gcc 624 Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala 205 195 200			
gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa cag ggc 672 Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly 220 210 215			
tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc ggt gat 720 Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val 235 225 230			
aca caa cca ctc tat ttt gac att aac gac agc tcg act gat gtg aac 768 Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn 255 245 250			
tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat ggc ttt 816 Tyr Leu Asn Glu Gln Gly Ile Thr Cys Val Asn His Asn Gly Phe 265 260 270			
cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc aag ttt 864 Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe 285 275 280			
gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att gca ggg 912 Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly 295 290 300			
gcg ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta gtg aaa 960			

Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys 1008  
 305 310 315 320  
 gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc aca aaa  
 Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys  
 325 330 335

ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt aac agt 1056  
 Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser  
 340 345 350

gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat tat cac 1104  
 Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His  
 355 360 365

cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att tct gat 1152  
 Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp  
 370 375 380

gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg ta 1190  
 Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser  
 385 390 395

<210> 115  
 <211> 396  
 <212> PRT  
 <213> Pasteurella multocida

<400> 115  
 Met Ser Glu Glu Tyr Leu His Gly Val Lys Val Thr Glu Ile Asn Gln  
 1 5 10 15  
 Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val  
 20 25 30  
 Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro  
 35 40 45  
 Val Leu Ile Thr Asn Val Ala Ala Ile Gly Lys 60 Ala Gly Lys Gln  
 50 55 60  
 Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys  
 65 70 75 80  
 Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu  
 85 90 95  
 Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu  
 100 105 110  
 Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys  
 115 120 125  
 Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys  
 130 135 140  
 Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe  
 145 150 155 160  
 Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln  
 165 170 175

Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp  
 180 185 190  
 Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala  
 195 200 205  
 Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly  
 210 215 220  
 Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val  
 225 230 235 240  
 Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn  
 245 250 255  
 Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe  
 260 265 270  
 Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe  
 275 280 285  
 Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly  
 290 295 300  
 Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys  
 305 310 315 320  
 Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys  
 325 330 335  
 Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser  
 340 345 350  
 Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His  
 355 360 365  
 Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp  
 370 375 380  
 Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser  
 385 390 395  
  
 <210> 116  
 <211> 2204  
 <212> DNA  
 <213> Pasteurella multocida  
  
 <220>  
 <223> unkK  
  
 <220>  
 <221> CDS  
 <222> (1)..(2202)  
  
 <400> 116  
 atg aat aaa aat cgc tat aaa ctc att ttt agt aaa act aaa ggc tgt 48  
 Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys  
 1 5 10 15  
 ctt gta cct gtt gct gaa acg att aat tct gca gta gga aat gcc tca 96  
 Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser  
 20 25 30

tca aaa gac gtt tct gac acc gag ata agt gct tct caa cca gcg ctc Ser Lys Asp Val Ser Asp Thr Glu Ile Ser Ala Ser Gln Pro Ala Leu 35 40 45	144
aac tcg ccg ctt tcg acc ctt tct gta tta gtc aaa acc gca ttt aat Asn Ser Pro Leu Ser Thr Leu Ser Val Leu Val Lys Thr Ala Phe Asn 50 55 60	192
ccg gtt tca aca ttg atg tcg ttg act tgg aaa gaa tac gcc gtt tta Pro Val Ser Thr Leu Met Ser Leu Thr Trp Lys Glu Tyr Ala Val Leu 65 70 75 80	240
tta tta agt gtg gtg tct ttt cct ctt atg gca caa gcc tct gat aca Leu Leu Ser Val Val Ser Phe Pro Leu Met Ala Gln Ala Ser Asp Thr 85 90 95	288
gat tca gtg gta caa aga aaa cct gaa tta act gat gtg acg aat agc Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser 100 105 110	336
aac agc tat cat gtg gaa tta gat aga gag cat cat aaa ggg gag cat Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His 115 120 125	384
caa aca aaa atc aaa cat act gag aat aat gtc atc att gtt gat att Gln Thr Lys Ile Lys His Thr Glu Asn Asn Val Ile Ile Val Asp Ile 130 135 140	432
gca aaa cca aac caa aag ggc att tca gat aac cgt ttt aaa cac ttc Ala Lys Pro Asn Gln Lys Gly Ile Ser Asp Asn Arg Phe Lys His Phe 145 150 155 160	480
aac atc cca aat ggg gcg gta ttt aac aat agc gcc aag gaa aaa cgc Asn Ile Pro Asn Gly Ala Val Phe Asn Asn Ser Ala Lys Glu Lys Arg 165 170 175	528
tca cag tta gtg ggg tat ttg cca ggt aac cag aat tta acg gaa ggt Ser Gln Leu Val Gly Tyr Leu Pro Gly Asn Gln Asn Leu Thr Glu Gly 180 185 190	576
agt gaa gca aaa gcg atc tta aat cag gtg act gga ccg gat gcc agt Ser Glu Ala Lys Ala Ile Leu Asn Gln Val Thr Gly Pro Asp Ala Ser 195 200 205	624
aaa att gaa ggc gcc ctt gaa att tta ggg caa aaa gcc gat ttg gtg Lys Ile Glu Gly Ala Leu Glu Ile Leu Gly Gln Lys Ala Asp Leu Val 210 215 220	672
att gcg aac caa aat ggc att gtg ctt aat ggg gta aaa acc att aat Ile Ala Asn Gln Asn Gly Ile Val Leu Asn Gly Val Lys Thr Ile Asn 225 230 235 240	720
gcc aat cgt ttt gtg gca aca acc agt agt acc att gat cct gag caa Ala Asn Arg Phe Val Ala Thr Thr Ser Ser Thr Ile Asp Pro Glu Gln 245 250 255	768
atg cag tta aat gtc acg caa ggt aca gtg aca att ggg gtg gat gga Met Gln Leu Asn Val Thr Gln Gly Thr Val Thr Ile Gly Val Asp Gly 260 265 270	816
ttt gcc aca gat ggc tta cct tat ttg gat atc att gcc aaa aag att Phe Ala Thr Asp Gly Leu Pro Tyr Leu Asp Ile Ile Ala Lys Lys Ile 275 280 285	864

gaa caa aaa caa gcg att aca aaa gaa aga aca gga aat tcc gaa acc 912 Glu Gln Lys Gln Ala Ile Thr Lys Glu Arg Thr Gly Asn Ser Glu Thr 290 295 300
gat atc act ttt gtc gca ggt aac agt aaa tat gat tta aag aca cat 960 Asp Ile Thr Phe Val Ala Gly Asn Ser Lys Tyr Asp Leu Lys Thr His 305 310 315 320
caa gtg aca gaa aag cat acc gct gag gca caa ggt gaa att gcg att 1008 Gln Val Thr Glu Lys His Thr Ala Glu Ala Gln Gly Glu Ile Ala Ile 325 330 335
agc ggt gcg agt acc ggt gca atg tac ggt aaa aat atc aaa tta atc 1056 Ser Gly Ala Ser Thr Gly Ala Met Tyr Gly Lys Asn Ile Lys Leu Ile 340 345 350
gta acg gat aaa ggc gct ggg gta aaa cat gat ggc att att tta tct 1104 Val Thr Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser 355 360 365
gag gcg gat att caa att gaa acc cat gag ggc gat gtt gaa tta ggc 1152 Glu Ala Asp Ile Gln Ile Glu Thr His Glu Gly Asp Val Glu Leu Gly 370 375 380
aat aca aaa aat aat cag aat gag aat tat gcc aaa gct cat gcg gaa 1200 Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu 385 390 395 400
ggg aat ttt acg gtt aaa ggc ggt aag cac gtt att att ggt aag gaa 1248 Gly Asn Phe Thr Val Lys Gly Gly Lys His Val Ile Ile Gly Lys Glu 405 410 415
gtt aaa gcc aac aaa gcg gtc gat att caa gca caa gaa aca aca gta 1296 Val Lys Ala Asn Lys Ala Val Asp Ile Gln Ala Gln Glu Thr Thr Val 420 425 430
aga caa aat gcg aaa tta act gcc aaa acg agt gcc aaa att aca gca 1344 Arg Gln Asn Ala Lys Leu Thr Ala Lys Thr Ser Ala Lys Ile Thr Ala 435 440 445
agt aag agt gtg aat ctt gaa gat aac gcg aaa ctt att gct aat gag 1392 Ser Lys Ser Val Asn Leu Glu Asp Asn Ala Lys Leu Ile Ala Asn Glu 450 455 460
ctg agc aca aca acc aat aaa tta acc aat aaa ggt agc att tac ggc 1440 Leu Ser Thr Thr Thr Asn Lys Leu Thr Asn Lys Gly Ser Ile Tyr Gly 465 470 475 480
aag aaa gtg acg cta gat gct gat aat tta gtc aat agt aaa gaa atc 1488 Lys Lys Val Thr Leu Asp Ala Asp Asn Leu Val Asn Ser Lys Glu Ile 485 490 495
tat gcg tct agc gaa ctt gat att caa acc aaa ggt cgt gat ctt tta 1536 Tyr Ala Ser Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu 500 505 510
ctt gag gat ggg gtt aat caa cca ctg agt ttc tta aaa ggc gct tca 1584 Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser 515 520 525
ttg tta gcg ccg ggg ttt gtc aac act ggg cta att cac agt aac ggt 1632 Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly 530 535 540

aat gcc aag ctc act ttt aaa gat gac acc agt ttt gtg act gaa gga 1680  
 Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly  
 545 550 555 560  
 aat aac ttt atc aca gca aaa gac aac tta gaa atc acg gca aaa aat 1728  
 Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn  
 565 570 575  
 gtt caa att gat caa gcg aaa aat att caa tta aac gcg aat atc acg 1776  
 Val Gln Ile Asp Gln Ala Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr  
 580 585 590  
 atc aat acc aag tct ggt ttt gtg aat tac ggt acc tta gca agt gct 1824  
 Ile Asn Thr Lys Ser Gly Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala  
 595 600 605  
 caa aat tta acg att aat acc gaa caa ggc agc att tat aac ata ggc 1872  
 Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly  
 610 615 620  
 ggt atc ttg ggg gcg ggt aaa agt ttg aat ctg agc gcg aaa aga gga 1920  
 Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly  
 625 630 635 640  
 gaa aac caa gga gga tat ctt att aat caa ggt aag agt cta ctc cat 1968  
 Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His  
 645 650 655  
 tct gaa ggc gcc atg aac ctc aca gcg gat cgc acg gtg tac aat tta 2016  
 Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu  
 660 665 670  
 ggg aat att ttt gct aaa ggt gac gcg acg atc aat gca aac gcg tta 2064  
 Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu  
 675 680 685  
 att aat gat gtt act ctc aca ggt cgt ctt gag tat caa gat ctg aaa 2112  
 Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys  
 690 695 700  
 aaa gat tat acg cgt tat tat cgt atc aat gaa acg gca aaa cat ggt 2160  
 Lys Asp Tyr Thr Arg Tyr Tyr Arg Ile Asn Glu Thr Ala Lys His Gly  
 705 710 715 720  
 tgg cat aat aac ttc tat gaa tta aac gtc gac aga gtt tct tg 2204  
 Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser  
 725 730

&lt;210&gt; 117

&lt;211&gt; 734

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 117

Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys  
 1 5 10 15  
 Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser  
 20 25 30  
 Ser Lys Asp Val Ser Asp Thr Glu Ile Ser Ala Ser Gln Pro Ala Leu  
 35 40 45

Asn Ser Pro Leu Ser Thr Leu Ser Val Leu Val Lys Thr Ala Phe Asn  
 50 55 60  
 Pro Val Ser Thr Leu Met Ser Leu Thr Trp Lys Glu Tyr Ala Val Leu  
 65 70 75 80  
 Leu Leu Ser Val Val Ser Phe Pro Leu Met Ala Gln Ala Ser Asp Thr  
 85 90 95  
 Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser  
 100 105 110  
 Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His  
 115 120 125  
 Gln Thr Lys Ile Lys His Thr Glu Asn Asn Val Ile Ile Val Asp Ile  
 130 135 140  
 Ala Lys Pro Asn Gln Lys Gly Ile Ser Asp Asn Arg Phe Lys His Phe  
 145 150 155 160  
 Asn Ile Pro Asn Gly Ala Val Phe Asn Asn Ser Ala Lys Glu Lys Arg  
 165 170 175  
 Ser Gln Leu Val Gly Tyr Leu Pro Gly Asn Gln Asn Leu Thr Glu Gly  
 180 185 190  
 Ser Glu Ala Lys Ala Ile Leu Asn Gln Val Thr Gly Pro Asp Ala Ser  
 195 200 205  
 Lys Ile Glu Gly Ala Leu Glu Ile Leu Gly Gln Lys Ala Asp Leu Val  
 210 215 220  
 Ile Ala Asn Gln Asn Gly Ile Val Leu Asn Gly Val Lys Thr Ile Asn  
 225 230 235 240  
 Ala Asn Arg Phe Val Ala Thr Thr Ser Ser Thr Ile Asp Pro Glu Gln  
 245 250 255  
 Met Gln Leu Asn Val Thr Gln Gly Thr Val Thr Ile Gly Val Asp Gly  
 260 265 270  
 Phe Ala Thr Asp Gly Leu Pro Tyr Leu Asp Ile Ile Ala Lys Lys Ile  
 275 280 285  
 Glu Gln Lys Gln Ala Ile Thr Lys Glu Arg Thr Gly Asn Ser Glu Thr  
 290 295 300  
 Asp Ile Thr Phe Val Ala Gly Asn Ser Lys Tyr Asp Leu Lys Thr His  
 305 310 315 320  
 Gln Val Thr Glu Lys His Thr Ala Glu Ala Gln Gly Glu Ile Ala Ile  
 325 330 335  
 Ser Gly Ala Ser Thr Gly Ala Met Tyr Gly Lys Asn Ile Lys Leu Ile  
 340 345 350  
 Val Thr Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser  
 355 360 365  
 Glu Ala Asp Ile Gln Ile Glu Thr His Glu Gly Asp Val Glu Leu Gly  
 370 375 380

Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu  
 385 390 395 400  
 Gly Asn Phe Thr Val Lys Gly Gly Lys His Val Ile Ile Gly Lys Glu  
 405 410 415  
 Val Lys Ala Asn Lys Ala Val Asp Ile Gln Ala Gln Glu Thr Thr Val  
 420 425 430  
 Arg Gln Asn Ala Lys Leu Thr Ala Lys Thr Ser Ala Lys Ile Thr Ala  
 435 440 445  
 Ser Lys Ser Val Asn Leu Glu Asp Asn Ala Lys Leu Ile Ala Asn Glu  
 450 455 460  
 Leu Ser Thr Thr Thr Asn Lys Leu Thr Asn Lys Gly Ser Ile Tyr Gly  
 465 470 475 480  
 Lys Lys Val Thr Leu Asp Ala Asp Asn Leu Val Asn Ser Lys Glu Ile  
 485 490 495  
 Tyr Ala Ser Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu  
 500 505 510  
 Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser  
 515 520 525  
 Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly  
 530 535 540  
 Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly  
 545 550 555 560  
 Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn  
 565 570 575  
 Val Gln Ile Asp Gln Ala Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr  
 580 585 590  
 Ile Asn Thr Lys Ser Gly Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala  
 595 600 605  
 Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly  
 610 615 620  
 Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly  
 625 630 635 640  
 Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His  
 645 650 655  
 Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu  
 660 665 670  
 Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu  
 675 680 685  
 Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys  
 690 695 700  
 Lys Asp Tyr Thr Arg Tyr Tyr Arg Ile Asn Glu Thr Ala Lys His Gly  
 705 710 715 720

Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser  
725 730

<210> 118  
<211> 251  
<212> DNA  
<213> *Pasteurella multocida*

<220>  
<223> unkO

<220>  
<221> CDS  
<222> (1)..(249)

<400> 118  
atg aaa att act att aca cga aat cat cca gaa gta ttt caa gaa tcc 48  
Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser  
1 5 10 15  
gct cgt tta gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca 96  
Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala  
20 25 30  
tta aca ttg gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt 144  
Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly  
35 40 45  
gag gag gaa agc aaa agg gga cat agt att aag gtt gta tta aaa gga 192  
Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly  
50 55 60  
agt cac gaa gtt att aag tca gag gtg aat aca aat gaa aaa aat cat 240  
Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His  
65 70 75 80  
tgt aat cat ta 251  
Cys Asn His

<210> 119  
<211> 83  
<212> PRT  
<213> *Pasteurella multocida*

<400> 119  
Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser  
1 5 10 15  
Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala  
20 25 30  
Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly  
35 40 45  
Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly  
50 55 60  
Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His  
65 70 75 80

Cys Asn His

&lt;210&gt; 120

&lt;211&gt; 548

&lt;212&gt; DNA

<213> *Pasteurella multocida*

&lt;220&gt;

&lt;223&gt; unkP

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(546)

&lt;400&gt; 120

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atg cgt gca tat ctt gat aaa gaa cag gcc tgg cat acg tct att tca 48
Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser
1 5 10 15

aat aaa gcc att aat gcc gtg agc ggt gtc aca caa cca ctc tat ttt 96
Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe
20 25 30

gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa gcc 144
Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly
35 40 45

atc acg tgt tgc gtg aat cat aat gcc ttt cgt ttt tgg gcc tta cgc 192
Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg
50 55 60

acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc act 240
Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr
65 70 75 80

gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca gtg 288
Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val
85 90 95

gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca atc 336
Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile
100 105 110

aat gcg aag tgg cgt gat tac acc aca aaa gcc tac tta att gcc ggt 384
Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly
115 120 125

aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa gat 432
Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp
130 135 140

gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc gaa 480
Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu
145 150 155 160

cag cta gcc ttt aat cag tac att tct gat gaa tac ctt gtt gat ttt 528
Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe
165 170 175

tca aat cgt tta gca tcg ta 548

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Ser Asn Arg Leu Ala Ser  
180

<210> 121

<211> 182

<212> PRT

<213> *Pasteurella multocida*

<400> 121

Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser  
1 5 10 15

Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe  
20 25 30

Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly  
35 40 45

Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg  
50 55 60

Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr  
65 70 75 80

Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val  
85 90 95

Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile  
100 105 110

Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly  
115 120 125

Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp  
130 135 140

Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu  
145 150 155 160

Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe  
165 170 175

Ser Asn Arg Leu Ala Ser  
180

<210> 122

<211> 69

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> apvA-or1

<220>

<221> CDS

<222> (1)..(69)

<400> 122

atg ttt tat gtc atg ctt gcc aat agg acg tct ata att tca tca atc 48  
Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile  
1 5 10 15

gat aag ttt aag ata ctt agc  
 Asp Lys Phe Lys Ile Leu Ser  
 20

69

<210> 123  
 <211> 23  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

<400> 123  
 Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile  
 1 5 10 15

Asp Lys Phe Lys Ile Leu Ser  
 20

<210> 124  
 <211> 64  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> apvA-or2

<220>  
 <221> CDS  
 <222> (3)..(62)

<400> 124  
 ag cta agt atc tta aac tta tcg att gat gaa att ata gac gtc cta 47  
 Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu  
 1 5 10 15

ttg gca agc atg aca ta 64  
 Leu Ala Ser Met Thr  
 20

<210> 125  
 <211> 20  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

<400> 125  
 Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu Leu  
 1 5 10 15

Ala Ser Met Thr  
 20

<210> 126  
 <211> 653  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> apvB

<220>  
 <221> CDS

&lt;222&gt; (1)..(651)

&lt;400&gt; 126

tta att agc ttt cct ttt att act ttt gca agt aat gtt aat gga gcc 48  
 Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala  
 1 5 10 15

gaa att gga ttg gga gga gcc cgt gag agt agt att tac tat tct aaa 96  
 Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys  
 20 25 30

cat aaa gta gca aca aat ccc ttt tta gca ctt gat ctt tct tta ggt 144  
 His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly  
 35 40 45

aat ttt tat atg aga ggg act gca gga att agc gaa ata gga tat gaa 192  
 Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu  
 50 55 60

caa tct ttc act gac aat ttc agc gta tca ctg ttt gtt aac cca ttt 240  
 Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe  
 65 70 75 80

gat ggt ttt tca att aaa gga aaa gac ttg tta cct gga tat caa agt 288  
 Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser  
 85 90 95

att caa act cgc aaa act caa ttt gcc ttt ggt tgg gga tta aat tat 336  
 Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr  
 100 105 110

aat ttg gga ggt tta ttc ggc tta aat gat act ttt ata tcc ttg gaa 384  
 Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu  
 115 120 125

gga aaa agc gga aaa cgt ggt gcg agt agt aat gtc agc tta ctt aaa 432  
 Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys  
 130 135 140

tcg ttt aat atg acg aaa aat tgg aaa gtt tca cca tat att ggc tca 480  
 Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser  
 145 150 155 160

agt tat tat tca tct aaa tat aca gat tat tac ttt ggt att aaa caa 528  
 Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln  
 165 170 175

tcc gaa tta ggt aat aaa att aca tcc gta tat aaa cct aaa gca gct 576  
 Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala  
 180 185 190

tat gca aca cac ata ggt att aat act gat tat gct ttc acg aac aat 624  
 Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn  
 195 200 205

ctt ggc atg ggt tta tct gtc ggt tgg at 653  
 Leu Gly Met Gly Leu Ser Val Gly Trp  
 210 215

&lt;210&gt; 127

&lt;211&gt; 217

&lt;212&gt; PRT

<213> Actinobacillus pleuropneumoniae

<400> 127

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Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala
 1             5             10             15

Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys
          20             25             30

His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly
          35             40             45

Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu
          50             55             60

Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe
          65             70             75             80

Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser
          85             90             95

Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr
          100            105            110

Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu
          115            120            125

Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys
          130            135            140

Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser
          145            150            155            160

Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln
          165            170            175

Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala
          180            185            190

Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn
          195            200            205

Leu Gly Met Gly Leu Ser Val Gly Trp
          210            215

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<210> 128

<211> 242

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> apvC

<220>

<221> CDS

<222> (1) .. (240)

<400> 128

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atg tgg cgg atg gga gat ttt atg tct aaa aaa gag agg ctg aat gat   48
Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp
 1             5             10             15

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atg gct cgc cag att tta tca gcg gcg gag ttg ctc att gca aag gaa 96
Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Ile Ala Lys Glu
      20                      25                      30

ggt ttg caa aat tta tcg atg agg aaa atc gca agt gaa gcc ggt atc 144
Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
      35                      40                      45

gca aca ggc acg ctt tat ctc tat ttc aaa acg aaa gac gag tta ctg 192
Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
      50                      55                      60

gat tgt ttg gcg gaa caa tta cat gaa cga tat tat cgt tat ctg aat 240
Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
      65                      70                      75                      80

at 242

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```

<210> 129
<211> 80
<212> PRT
<213> Actinobacillus pleuropneumoniae

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```

<400> 129
Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp
      1                      5                      10                      15

Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Leu Ile Ala Lys Glu
      20                      25                      30

Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
      35                      40                      45

Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
      50                      55                      60

Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
      65                      70                      75                      80

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<210> 130
<211> 527
<212> DNA
<213> Actinobacillus pleuropneumoniae

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<220>
<223> apvD

```

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<220>
<221> CDS
<222> (1)..(525)

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<400> 130
aat att caa aaa aca gtt att gct agc ggc aca ttg caa gcg act gaa 48
Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu
      1                      5                      10                      15

caa gta gat att ggt gca caa gta tct ggg cag att aag cat att tta 96
Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu
      20                      25                      30

gta caa gaa gga cag aag gtt aaa aaa ggt gag cta tta gct gta att 144

```

Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile  
 35 40 45

gat cca cgt ctg gct gaa acg gaa tta aaa cta gca aaa gct gag cta 192  
 Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu  
 50 55 60

gca aat gct tct gct aat ttg gat aca aaa aaa att aat ctt aag caa 240  
 Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln  
 65 70 75 80

ctg caa tca gat tgg gaa cgt cat caa cgt ttg ata cga acc aat gcg 288  
 Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala  
 85 90 95

aca agc caa aag gaa aca gaa gaa gca aaa agt aga tta aat acg gcc 336  
 Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala  
 100 105 110

aaa gca gaa ctt caa att gcg caa aat aat cta gat atc gct aaa atc 384  
 Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile  
 115 120 125

aga gtg gaa aaa gct gaa acc gaa cta gga tat aca gaa att cgt tct 432  
 Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser  
 130 135 140

cca ctt gat gca aca gta att tca gta ttt gcg caa aat ggt caa act 480  
 Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr  
 145 150 155 160

tta gtc acc acc caa caa gta cca gtg ctg atg aaa tta gct aat at 527  
 Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn  
 165 170 175

&lt;210&gt; 131

&lt;211&gt; 175

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 131

Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu  
 1 5 10 15

Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu  
 20 25 30

Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile  
 35 40 45

Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu  
 50 55 60

Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln  
 65 70 75 80

Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala  
 85 90 95

Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala  
 100 105 110

Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile  
 115 120 125  
 Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser  
 130 135 140  
 Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr  
 145 150 155 160  
 Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn  
 165 170 175

<210> 132

<211> 867

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> atpG

<220>

<221> CDS

<222> (1) .. (864)

<400> 132

atg gca ggt gcg aaa gag ata aga acc aaa att gca agt gtg aaa aat 48  
 Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn  
 1 5 10 15  
 act caa aaa atc acc aaa gca atg gaa atg gtt gct acc tct aaa atg 96  
 Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met  
 20 25 30  
 cgt aaa acg caa gag cgt atg gct gcc agt cgt cct tat tcg gaa aca 144  
 Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr  
 35 40 45  
 atc cgt aag gtg att agc cat att gcg aaa gga agc att ggt tat aag 192  
 Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys  
 50 55 60  
 cac ccg ttt tta act gaa cgt gat att aaa aaa gta ggc tat ctt gtc 240  
 His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val  
 65 70 75 80  
 gtt tcg acc gat cgc ggt tta tgc ggt ggc ctt aat atc aat tta ttc 288  
 Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe  
 85 90 95  
 aaa gcg act ttg aat gaa ttt aaa acg tgg aaa gat aaa gac gtt agt 336  
 Lys Ala Thr Leu Asn Glu Phe Lys Thr Trp Lys Asp Lys Asp Val Ser  
 100 105 110  
 gtt gag ctt ggt tta gta ggg tcg aaa ggc gta agc ttt tac caa aat 384  
 Val Glu Leu Gly Leu Val Gly Ser Lys Gly Val Ser Phe Tyr Gln Asn  
 115 120 125  
 cta ggc tta aac gtg aga tct caa gta acg gga tta ggc gat aat ccg 432  
 Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro  
 130 135 140  
 gaa atg gaa cgt atc gtg ggc gca gtt aat gaa atg att aat gcg ttc 480

Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe  
 145 150 155 160  
 cga aac gga gaa gtg gat gcg gtt tac gtc gct tac aac cgt ttt gaa 528  
 Arg Asn Gly Glu Val Asp Ala Val Tyr Val Ala Tyr Asn Arg Phe Glu  
 165 170 175  
 aat acg atg tca caa aaa cct gtt atc gca cag tta ctt ccg tta cct 576  
 Asn Thr Met Ser Gln Lys Pro Val Ile Ala Gln Leu Leu Pro Leu Pro  
 180 185 190  
 aaa cta gat gac gat gaa tta gat acg aaa ggt tca tgg gat tat att 624  
 Lys Leu Asp Asp Asp Glu Leu Asp Thr Lys Gly Ser Trp Asp Tyr Ile  
 195 200 205  
 tat gaa ccg aat cca caa gtt tta ttg gat agt tta ctt gtt cgt tat 672  
 Tyr Glu Pro Asn Pro Gln Val Leu Leu Asp Ser Leu Leu Val Arg Tyr  
 210 215 220  
 tta gaa act cag gta tac caa gca gtt gta gat aac cta gct tct gaa 720  
 Leu Glu Thr Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu  
 225 230 235 240  
 caa gcc gct cga atg gta gcg atg aaa gcc gca aca gat aat gcg ggt 768  
 Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly  
 245 250 255  
 aca tta atc gat gaa tta caa tta gtg tat aac aaa gct cgc caa gca 816  
 Thr Leu Ile Asp Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala  
 260 265 270  
 agc att aca aat gaa tta aac gaa att gtt gcg ggt gcc gca gca att 864  
 Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile  
 275 280 285  
 taa 867  
  
 <210> 133  
 <211> 288  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae  
  
 <400> 133  
 Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn  
 1 5 10 15  
 Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met  
 20 25 30  
 Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr  
 35 40 45  
  
 Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys  
 50 55 60  
 His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val  
 65 70 75 80  
 Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe  
 85 90 95

Lys Ala Thr Leu Asn Glu Phe Lys Thr Trp Lys Asp Lys Asp Val Ser  
 100 105 110  
 Val Glu Leu Gly Leu Val Gly Ser Lys Gly Val Ser Phe Tyr Gln Asn  
 115 120 125  
 Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro  
 130 135 140  
 Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe  
 145 150 155 160  
 Arg Asn Gly Glu Val Asp Ala Val Tyr Val Ala Tyr Asn Arg Phe Glu  
 165 170 175  
 Asn Thr Met Ser Gln Lys Pro Val Ile Ala Gln Leu Leu Pro Leu Pro  
 180 185 190  
 Lys Leu Asp Asp Asp Glu Leu Asp Thr Lys Gly Ser Trp Asp Tyr Ile  
 195 200 205  
 Tyr Glu Pro Asn Pro Gln Val Leu Leu Asp Ser Leu Leu Val Arg Tyr  
 210 215 220  
 Leu Glu Thr Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu  
 225 230 235 240  
 Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly  
 245 250 255  
 Thr Leu Ile Asp Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala  
 260 265 270  
 Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile  
 275 280 285

<210> 134  
 <211> 534  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> atpH

<220>  
 <221> CDS  
 <222> (1)..(531)

<400> 134  
 atg tca gaa tta agt aca gta gct cgc ccc tac gct aaa gca gct ttt 48  
 Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe  
 1 5 10 15  
 gat ttt gct tta gaa caa ggt cag ttg gac aaa tgg caa gaa atg tta 96  
 Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu  
 20 25 30  
 cag ttt tgg gca ttc gtt gct gaa aac gaa caa gtg gcg gaa tat att 144  
 Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile  
 35 40 45  
 aat tct tcc ctt gca agc ggt cag att tct gaa act ttt atc aaa atc 192

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Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile
  50                      55                      60
tgc ggc gac caa ctt gat caa tat ggg caa aat ttt att cgt gta atg   240
Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met
  65                      70                      75                      80
gct gaa aat aaa cgt ctg gct gtg ttg cct atg gtt ttt gat act ttc   288
Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe
  85                      90                      95
gta tca tta cga gcg gaa cat gaa gcg gta aaa gat gta aca att gtt   336
Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val
  100                     105                     110
tcg gca aac gaa tta agt caa gca caa gaa gat aaa atc gca aaa gcg   384
Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala
  115                     120                     125
atg gaa aaa cgc tta ggt caa aaa gtt cgt tta acc aac caa atc gat   432
Met Glu Lys Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp
  130                     135                     140
aac agc ctg att gca gcg gta att att aaa tac gat gat gtt gtt att   480
Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile
  145                     150                     155                     160
gat ggt agt agc cgc ggt cag tta aat cgc tta gcg tca gcg ttg agc   528
Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser
  165                     170                     175
ttg taa
Leu
534

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&lt;210&gt; 135

&lt;211&gt; 177

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 135

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Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
  1                      5                      10                      15

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Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu
  20                      25                      30

```

```

Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile
  35                      40                      45

```

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Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile
  50                      55                      60

```

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Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met
  65                      70                      75                      80

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Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe
  85                      90                      95

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Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val
  100                     105                     110

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Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala
    115                                120                                125

Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp
    130                                135                                140

Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile
    145                                150                                155                                160

Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser
    165                                170                                175

Leu

```

&lt;210&gt; 136

&lt;211&gt; 321

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; dksA

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(318)

&lt;400&gt; 136

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gca tgg cat gtg caa att atg gac gaa gct gag cgt aca aaa aac caa   48
Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
    1                                5                                10                                15

atg cag gaa gaa gtc gct aat ttc gcc gat cct gcg gac cgc gcc act   96
Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
    20                                25                                30

cag gaa gaa gaa ttc agt ctt gaa tta aga aac cgt gac cgt gag cgt   144
Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg
    35                                40                                45

aaa ttg ctt aag aag att gag caa acg tta aat agc att gcc gaa gac   192
Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp
    50                                55                                60

gaa tac ggc tat tgc gaa act tgc ggt gtt gaa atc ggt tta cgt cgt   240
Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg
    65                                70                                75                                80

tta gaa gcg cgc ccg acc gcg gat atg tgt atc gat tgc aaa aca ctt   288
Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu
    85                                90                                95

gcg gaa atc cgt gaa aag caa atg ggc tta taa   321
Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
    100                                105

```

&lt;210&gt; 137

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 137

Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln  
 1 5 10 15

Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr  
 20 25 30

Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg  
 35 40 45

Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp  
 50 55 60

Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg  
 65 70 75 80

Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu  
 85 90 95

Ala Glu Ile Arg Glu Lys Gln Met Gly Leu  
 100 105

&lt;210&gt; 138

&lt;211&gt; 33

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; dnaK

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (30)

&lt;400&gt; 138

gct gag ttt gaa gaa gtg aaa gat aat aaa taa

33

Ala Glu Phe Glu Glu Val Lys Asp Asn Lys  
 1 5 10

&lt;210&gt; 139

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 139

Ala Glu Phe Glu Glu Val Lys Asp Asn Lys  
 1 5 10

&lt;210&gt; 140

&lt;211&gt; 453

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; exbB

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (450)

<400> 140  
 atg gaa caa atg ctt gaa ctt tta caa ggt cat gtt gat tat att att 48  
 Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile  
 1 5 10 15

tta ggc tta tta cta tta atg agt gtt gtg ttg gta tgg aaa att att 96  
 Leu Gly Leu Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile  
 20 25 30

gaa cgc gta ctt ttc tac aaa caa ttg gat gtg acc aaa tat gac acg 144  
 Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr  
 35 40 45

cta caa gat ttg gaa att gat acc act cgc aat tta acc acc att tcc 192  
 Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser  
 50 55 60

act atc ggt gcc aac gcc cct tat atc ggt tta tta gga acc gta tta 240  
 Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu  
 65 70 75 80

ggg atc tta ctt acc ttc tat cat tta ggg cat tcc ggc ggt gat att 288  
 Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile  
 85 90 95

gac gcc gca tcc att atg gtt cac ctt tgc ctt gca tta aaa gca acc 336  
 Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr  
 100 105 110

gca gcc ggt atc tta gtc gct att ccg gca atg atg ttc tac agc ggt 384  
 Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly  
 115 120 125

ttt aac cgt aaa gtg gat gaa agc aaa ctt aaa tgg caa gcg att caa 432  
 Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln  
 130 135 140

gct cgt aaa gcc aat caa taa 453  
 Ala Arg Lys Ala Asn Gln  
 145 150

&lt;210&gt; 141

&lt;211&gt; 150

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 141

Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile  
 1 5 10 15

Leu Gly Leu Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile  
 20 25 30

Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr  
 35 40 45

Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser  
 50 55 60

Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu  
 65 70 75 80

[illegible]

&lt;210&gt; 142

<211> 720

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

**<220>**

**<223> fkpA**

**<220>**

<221> CDS

<222> (1) .. (717)

&lt;400&gt; 142

atg tta aaa aat aaa ctt tct gtt ctt gca atc gta gcc ggt acg ttc 48  
Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe  
1 5 10 15

ggt tca gct caa act gca ttt gca gcg gat caa aaa ttc att gac gat 96  
Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp  
20 25 30

tca tca tat gca gtc ggc gta ttg atg ggt aaa aat atc gaa ggc gtc 144  
Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val  
35 40 45

ggt gaa tca caa aaa gaa att ttt tct tat aac caa gat aaa atc ttg 192  
Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu  
50 55 60

gcg ggt gtc caa gat acc atc aaa aaa acc ggt aaa tta acc gat gaa 240  
Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu  
65 70 75 80

gat cta caa aaa caa tta aaa tcg ctt gat act tat ctt gca agt caa 288  
Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln  
85 90 95

gaa agc aaa att gcg gcg gag aaa agc aaa gca acc gta gaa gcc ggt 336  
Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly  
100 105 110

aat aaa ttt cgt acc gac tac gaa aaa caa agc ggc gtg aaa aaa acc 384  
Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr  
115 120 125

gct tcc ggt tta ctt tat aaa att gaa aaa gcc qqc acq qqc qaa tcq 432

Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser  
 130 135 140

cct aaa gcg gaa gat acc gtt aaa gtt cac tat aaa ggg aca tta acc 480  
 Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr  
 145 150 155 160

gat ggt acg gta ttc gat agc tca tac gat cgc ggt gag ccg att gaa 528  
 Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu  
 165 170 175

ttc caa tta aac caa tta att ccg ggt tgg att gaa gcg att cca atg 576  
 Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met  
 180 185 190

ttg aaa aaa ggc gga aaa atg gaa atc gtc gtt ccg cct gaa ctt ggt 624  
 Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly  
 195 200 205

tac ggc gaa cgc caa gca ggt aag att ccg gca agt tca acc tta aaa 672  
 Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys  
 210 215 220

ttc gag att gaa ttg tta gat ttc aaa gcg gcc gaa gcg aaa aaa taa 720  
 Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys  
 225 230 235

<210> 143  
 <211> 239  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

<400> 143  
 Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe  
 1 5 10 15

Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp  
 20 25 30

Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val  
 35 40 45

Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu  
 50 55 60

Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu  
 65 70 75 80

Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln  
 85 90 95

Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly  
 100 105 110

Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr  
 115 120 125

Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser  
 130 135 140

Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr  
 145 150 155 160

Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu  
 165 170 175

Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met  
 180 185 190

Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly  
 195 200 205

Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys  
 210 215 220

Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys  
 225 230 235

&lt;210&gt; 144

&lt;211&gt; 290

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; HI0379

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (3) .. (287)

&lt;400&gt; 144

tg cat agc gtg aga ggt ccg ggc ggc ggt tat caa ctc ggt aag caa	47
His Ser Val Arg Gly Pro Gly Gly Gly Tyr Gln Leu Gly Lys Gln	
1 5 10 15	
cct gaa gag att agt gtg ggg atg att att gcg gcg gtg aat gaa aat	95
Pro Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn	
20 25 30	
ctc gac gta acc aaa tgt aaa ggt agc ggc aac tgt agc aaa aac tct	143
Leu Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser	
35 40 45	
cag tgc tta acc cat cat tta tgg gaa cgt tta gaa gaa caa atc ggt	191
Gln Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly	
50 55 60	
gtg ttt tta aat acg att act tta gcg gaa ctt gtt gaa gaa cat tcg	239
Val Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser	
65 70 75	
gat cac gat tgt gaa aaa gaa cat tgc cac gat cat tca cac aaa cat	287
Asp His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His	
80 85 90 95	
taa	290

&lt;210&gt; 145

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 145

His Ser Val Arg Gly Gly Gly Tyr Gln Leu Gly Lys Gln Pro

1	5	10	15
Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn Leu	20	25	30
Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser Gln	35	40	45
Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly Val	50	55	60
Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser Asp	65	70	75
His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His	85	90	95

&lt;210&gt; 146

&lt;211&gt; 273

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; hupa

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(270)

&lt;400&gt; 146

atg aac aaa act gag tta atc gat gca atc gca gct ggt gca gag tta	48
Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu	
1 5 10 15	
agc aag aaa gac gcg aaa gcg gca tta gaa gcg act tta aat gcg atc	96
Ser Lys Lys Asp Ala Lys Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile	
20 25 30	
tct gaa agc cta aaa aat ggc gac acc gtt cag tta atc ggc ttc ggt	144
Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly	
35 40 45	
act ttt aaa gta aac gag cgt aat gca cgt acg ggt cgt aac ccg cgt	192
Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg	
50 55 60	
acc ggc gaa gaa atc aaa atc gca gca tct aaa gtg ccg gcg ttt gtt	240
Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val	
65 70 75 80	
gca ggt aaa gca tta aaa gat tta gta aaa taa	273
Ala Gly Lys Ala Leu Lys Asp Leu Val Lys	
85 90	

&lt;210&gt; 147

&lt;211&gt; 90

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 147

Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu

1	5	10	15
Ser Lys Lys Asp Ala Lys Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile	20	25	30
Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly	35	40	45
Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg	50	55	60
Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val	65	70	75
Ala Gly Lys Ala Leu Lys Asp Leu Val Lys	85	90	

&lt;210&gt; 148

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; lpdA

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(549)

&lt;400&gt; 148

atg agc aaa gaa atc aaa acg caa gtc gtg gta ctt ggt gcg ggt cct	48
Met Ser Lys Glu Ile Lys Thr Gln Val Val Leu Gly Ala Gly Pro	
1 5 10 15	
gcc ggt tat tca gcg gca ttc cgt tgt gcc gac tta ggc tta gaa aca	96
Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr	
20 25 30	
gta att gtc gaa cgt tat tca act ttg ggc ggt gta tgc tta aac gta	144
Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val	
35 40 45	
ggc tgt att ccg tct aaa gca tta tta cac gtt gca aaa gtt atc gaa	192
Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu	
50 55 60	
gaa gca aaa cac gca gag aaa aac ggt att act ttc ggt gag ccc aac	240
Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn	
65 70 75 80	
att gat tta gat aaa gtg cgt gcg ggt aaa gaa gcg gtt gtt tct aaa	288
Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys	
85 90 95	
tta acc ggc ggt tta gcg ggt atg gct aaa gca cgt aaa gta aca gta	336
Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val	
100 105 110	
gtg gaa ggt tta gcg gcg ttt acc gat ccg aat act tta gta gct cgt	384
Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg	
115 120 125	

gac cgt gac ggt aat ccg aca acg att aaa ttt gat tat gca att att 432  
 Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile  
 130 135 140

gca gcc ggt tct cgt ccg att cag ctt ccg ttc att cca cac gaa gat 480  
 Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp  
 145 150 155 160

ccg cgt gtg tgg gat tct acg gat gca ctt aaa tta aaa gaa gta ccc 528  
 Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro  
 165 170 175

gaa aaa att act cat tat ggg cc 551  
 Glu Lys Ile Thr His Tyr Gly  
 180

<210> 149

<211> 183

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 149

Met Ser Lys Glu Ile Lys Thr Gln Val Val Val Leu Gly Ala Gly Pro  
 1 5 10 15

Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr  
 20 25 30

Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val  
 35 40 45

Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu  
 50 55 60

Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn  
 65 70 75 80

Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys  
 85 90 95

Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val  
 100 105 110

Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg  
 115 120 125

Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile  
 130 135 140

Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp  
 145 150 155 160

Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro  
 165 170 175

Glu Lys Ile Thr His Tyr Gly  
 180

<210> 150

<211> 1095

<212> DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; Omp5-2

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (1092)

&lt;400&gt; 150

atg aaa aaa tca tta gtt gct tta aca gta tta tcg gct gca gcg gta	48
Met Lys Lys Ser Leu Val Ala Leu Thr Val Leu Ser Ala Ala Ala Val	
1 5 10 15	
gct caa gca gcg cca caa caa aat act ttc tac gca ggt gcg aaa gca	96
Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Ala	
20 25 30	
ggc tgg gcg tca ttc cat gat ggt atc gaa caa tta gat tca gct aaa	144
Gly Trp Ala Ser Phe His Asp Gly Ile Glu Gln Leu Asp Ser Ala Lys	
35 40 45	
aac aca gat cgc ggt aca aaa tac ggt atc aac cgt aat tca gta act	192
Asn Thr Asp Arg Gly Thr Lys Tyr Gly Ile Asn Arg Asn Ser Val Thr	
50 55 60	
tac ggc gta ttc ggc ggt tac caa att tta aac caa gac aaa tta ggt	240
Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly	
65 70 75 80	
tta gcg gct gaa tta ggt tat gac tat ttc ggt cgt gtg cgc ggt tct	288
Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser	
85 90 95	
gaa aaa cca aac ggt aaa gcg gac aag aaa act ttc cgt cac gct gca	336
Glu Lys Pro Asn Gly Lys Ala Asp Lys Lys Thr Phe Arg His Ala Ala	
100 105 110	
cac ggt gcg aca atc gca tta aaa cct agc tac gaa gta tta cct gac	384
His Gly Ala Thr Ile Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp	
115 120 125	
tta gac gtt tac ggt aaa gta ggt atc gca tta gta aac aat aca tat	432
Leu Asp Val Tyr Gly Lys Val Gly Ile Ala Leu Val Asn Asn Thr Tyr	
130 135 140	
aaa aca ttc aat gca gca caa gag aaa gtg aaa act cgt cgt ttc caa	480
Lys Thr Phe Asn Ala Ala Gln Glu Lys Val Lys Thr Arg Arg Phe Gln	
145 150 155 160	
agt tct tta att tta ggt gcg ggt gtt gag tac gca att ctt cct gaa	528
Ser Ser Leu Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro Glu	
165 170 175	
tta gcg gca cgt gtt gaa tac caa tgg tta aac aac gca ggt aaa gca	576
Leu Ala Ala Arg Val Glu Tyr Gln Trp Leu Asn Asn Ala Gly Lys Ala	
180 185 190	
agc tac tct act tta aat cgt atg ggt gca act gac tac cgt tcg gat	624
Ser Tyr Ser Thr Leu Asn Arg Met Gly Ala Thr Asp Tyr Arg Ser Asp	
195 200 205	

atc agt tcc gta tct gca ggt tta agc tac cgt ttc ggt caa ggt gcg 672  
 ile ser ser val ser ala gly leu ser tyr arg phe gly gln gly ala  
 210 215 220  
 gca ccg gtt gca gct ccg gca gtt gaa act aaa aac ttc gca ttc agc 720  
 ala pro val ala ala pro ala val glu thr lys asn phe ala phe ser  
 225 230 235 240  
 tct gac gta tta ttc gca ttc ggt aaa tca aac tta aaa ccg gct gcg 768  
 ser asp val leu phe ala phe gly lys ser asn leu lys pro ala ala  
 245 250 255  
 gca aca gca tta gat gca atg caa acc gaa atc aat aac gca ggt tta 816  
 ala thr ala leu asp ala met gln thr glu ile asn asn ala gly leu  
 260 265 270  
 tca aat gct gcg atc caa gta aac ggt tac acg gac cgt atc ggt aaa 864  
 ser asn ala ala ile gln val asn gly tyr thr asp arg ile gly lys  
 275 280 285  
 gaa gct tca aac tta aaa ctt tca caa cgt cgt gcg gaa aca gta gct 912  
 glu ala ser asn leu lys leu ser gln arg arg ala glu thr val ala  
 290 295 300  
 aac tac atc gtt tct aaa ggt gct ccg gca gct aac gta act gca gta 960  
 asn tyr ile val ser lys gly ala pro ala ala asn val thr ala val  
 305 310 315 320  
 ggt tac ggt gaa gca aac cct gta acc ggc gca aca tgt gac aaa gtt 1008  
 gly tyr gly glu ala asn pro val thr gly ala thr cys asp lys val  
 325 330 335  
 aaa ggt cgt aaa gca tta atc gct tgc tta gca ccg gat cgt cgt gtt 1056  
 lys gly arg lys ala leu ile ala cys leu ala pro asp arg arg val  
 340 345 350  
 gaa gtt caa gtt caa ggt act aaa gaa gta act atg taa 1095  
 glu val gln val gln gly thr lys glu val thr met  
 355 360  
 <210> 151  
 <211> 364  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae  
 <400> 151  
 Met Lys Lys Ser Leu Val Ala Leu Thr Val Leu Ser Ala Ala Ala Val  
 1 5 10 15  
 Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Ala  
 20 25 30  
 Gly Trp Ala Ser Phe His Asp Gly Ile Glu Gln Leu Asp Ser Ala Lys  
 35 40 45  
 Asn Thr Asp Arg Gly Thr Lys Tyr Gly Ile Asn Arg Asn Ser Val Thr  
 50 55 60  
 Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly  
 65 70 75 80  
 Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser

85										90										95																																		
Glu	Lys	Pro	Asn	Gly	Lys	Ala	Asp	Lys	Lys	Thr	Phe	Arg	His	Ala	Ala																																							
			100						105					110																																								
His	Gly	Ala	Thr	Ile	Ala	Leu	Lys	Pro	Ser	Tyr	Glu	Val	Leu	Pro	Asp																																							
			115					120					125																																									
Leu	Asp	Val	Tyr	Gly	Lys	Val	Gly	Ile	Ala	Leu	Val	Asn	Asn	Thr	Tyr																																							
			130				135					140																																										
Lys	Thr	Phe	Asn	Ala	Ala	Gln	Glu	Lys	Val	Lys	Thr	Arg	Arg	Phe	Gln																																							
					150					155				160																																								
Ser	Ser	Leu	Ile	Leu	Gly	Ala	Gly	Val	Glu	Tyr	Ala	Ile	Leu	Pro	Glu																																							
				165					170					175																																								
Leu	Ala	Ala	Arg	Val	Glu	Tyr	Gln	Trp	Leu	Asn	Asn	Ala	Gly	Lys	Ala																																							
			180					185					190																																									
Ser	Tyr	Ser	Thr	Leu	Asn	Arg	Met	Gly	Ala	Thr	Asp	Tyr	Arg	Ser	Asp																																							
			195				200					205																																										
Ile	Ser	Ser	Val	Ser	Ala	Gly	Leu	Ser	Tyr	Arg	Phe	Gly	Gln	Gly	Ala																																							
			210			215				220																																												
Ala	Pro	Val	Ala	Ala	Pro	Ala	Val	Glu	Thr	Lys	Asn	Phe	Ala	Phe	Ser																																							
			225			230			235					240																																								
Ser	Asp	Val	Leu	Phe	Ala	Phe	Gly	Lys	Ser	Asn	Leu	Lys	Pro	Ala	Ala																																							
			245					250					255																																									
Ala	Thr	Ala	Leu	Asp	Ala	Met	Gln	Thr	Glu	Ile	Asn	Asn	Ala	Gly	Leu																																							
			260				265					270																																										
Ser	Asn	Ala	Ala	Ile	Gln	Val	Asn	Gly	Tyr	Thr	Asp	Arg	Ile	Gly	Lys																																							
			275				280					285																																										
Glu	Ala	Ser	Asn	Leu	Lys	Leu	Ser	Gln	Arg	Arg	Ala	Glu	Thr	Val	Ala																																							
			290			295					300																																											
Asn	Tyr	Ile	Val	Ser	Lys	Gly	Ala	Pro	Ala	Ala	Asn	Val	Thr	Ala	Val																																							
			305			310			315					320																																								
Gly	Tyr	Gly	Glu	Ala	Asn	Pro	Val	Thr	Gly	Ala	Thr	Cys	Asp	Lys	Val																																							
			325					330				335																																										
Lys	Gly	Arg	Lys	Ala	Leu	Ile	Ala	Cys	Leu	Ala	Pro	Asp	Arg	Arg	Val																																							
			340				345					350																																										
Glu	Val	Gln	Val	Gln	Gly	Thr	Lys	Glu	Val	Thr	Met																																											
			355				360																																															

&lt;210&gt; 152

&lt;211&gt; 1110

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; Omp5

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (1107)

&lt;400&gt; 152

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atg aaa aaa tca tta gtt gct tta gca gta tta tcg gct gca gca gta 48
Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Ala Val
      1              5              10              15

gct caa gca gct cca caa caa aat act ttc tac gca ggt gcg aaa gtt 96
Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val
      20              25              30

ggg caa tca tca ttt cac cac ggt gtt aac caa tta aaa tct ggt cac 144
Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His
      35              40              45

gat gat cgt tat aat gat aaa aca cgt aag tat ggt atc aac cgt aac 192
Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn
      50              55              60

tct gta act tac ggt gta ttc ggc ggt tac caa atc tta aac caa aat 240
Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn
      65              70              75

aac ttc ggt tta gca gct gaa tta ggc tat gac tac tac ggt cgc gta 288
Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Asp Tyr Tyr Gly Arg Val
      85              90              95

cgt ggt aac gta gat gaa ttc cgt aca gtt aaa cac tct gct cac ggt 336
Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly
      100             105             110

tta aac tta gcg tta aaa cca agc tac gaa gta tta cct gac tta gac 384
Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp
      115             120             125

gtt tac ggt aaa gta ggt att gcg gtt gtt cgt aat gac tat aaa aaa 432
Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys
      130             135             140

tat ggt gcg gaa aac act aac gaa tca aca aca aaa ttc cac aaa tta 480
Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu
      145             150             155

aaa gca tca act att tta ggt gca ggt gtt gag tac gca att ctt cct 528
Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro
      165             170             175

gaa tta gcg gca cgt gtt gaa tac caa tac tta aac aaa gcg ggt aac 576
Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn
      180             185             190

tta aat aaa gca tta gtt cgt tca ggc aca caa gat gtg gac ttc caa 624
Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln
      195             200             205

tat gct cct gat atc cac tct gta aca gca ggt tta tca tac cgt ttc 672
Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe
      210             215             220

ggg caa ggc gct gta gca cca gtt gtt gag cca gaa gtt gta act aaa 720
Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys
      225             230             235

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aac ttc gca ttc agc tca gac gtt tta ttt gat ttc ggt aaa tca agc 768
Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser
      245                                250                                255

tta aaa cca gca gca gca aca gct tta gac gca gct aac act gaa atc 816
Leu Lys Pro Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile
      260                                265                                270

gct aac tta ggt tta gca act cca gct atc caa gtt aac ggt tat aca 864
Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr
      275                                280                                285

gac cgt atc ggt aaa gaa gct tca aac tta aaa ctt tca caa cgc cgt 912
Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg
      290                                295                                300

gca gaa act gta gct aac tac tta gtt tct aaa ggt caa aac cct gca 960
Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala
      305                                310                                315                                320

aac gta act gca gta ggt tac ggt gaa gca aac cca gta acc ggc gca 1008
Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala
      325                                330                                335

aca tgt gat gca gtt aaa ggt cgt aaa gca tta atc gct tgc tta gca 1056
Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala
      340                                345                                350

ccg gat cgt cgt gtt gaa gtt caa gta caa ggt gct aaa aac gta gct 1104
Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala
      355                                360                                365

atg taa 1110
Met

<210> 153
<211> 369
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 153
Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Ala Val
  1      5      10      15

Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val
  20      25      30

Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His
  35      40      45

Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn
  50      55      60

Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn
  65      70      75      80

Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Tyr Gly Arg Val
  85      90      95

Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly
  100     105     110

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Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp  
 115 120 125  
 Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys  
 130 135 140  
 Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu  
 145 150 155 160  
 Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro  
 165 170 175  
 Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn  
 180 185 190  
 Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln  
 195 200 205  
 Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe  
 210 215 220  
 Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys  
 225 230 235 240  
 Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser  
 245 250 255  
 Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile  
 260 265 270  
 Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr  
 275 280 285  
 Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg  
 290 295 300  
 Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala  
 305 310 315 320  
 Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala  
 325 330 335  
 Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala  
 340 345 350  
 Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala  
 355 360 365

Met

&lt;210&gt; 154

&lt;211&gt; 1076

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; pnp new

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1074)

<400> 154  
aat att aaa gaa ttc gta aaa gaa gcg ggt aaa ccg cgt tgg gat tgg 48  
Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp  
1 5 10 15

gtt gcg ccg gaa ccg aat acc gca tta atc aac caa gtt aaa gcg tta 96  
Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu  
20 25 30

gcg gaa gcg cgt atc ggc gat ccg tat cgt att aca gaa aaa caa gcg 144  
Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala  
35 40 45

cgt tac gaa caa atc gat gca att aaa gcg gat gtt atc gca caa tta 192  
Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu  
50 55 60

acc gca caa gac gaa acc gtt tct gaa ggt gcg att att gat att att 240  
Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile  
65 70 75 80

acc gca tta gaa agt tct att gtt gcg ggt cgt att att gcc gcc gaa 288  
Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu  
85 90 95

ccg cgt att gac ggt cgt acg gta gat acg gtt cgt gca tta gac att 336  
Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile  
100 105 110

tgc acc gcc gta tta cct cgt acg cac ggt tct gca atc ttt act gcg 384  
Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg  
115 120 125

ggt gaa aca caa gca tta gcg gtt gca acc tta ggt act gag cgc gat 432  
Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp  
130 135 140

gca caa att gtt gac gaa tta acc gcc gag aaa tca gac cgt ttc tta 480  
Ala Gln Ile Val Asp Glu Leu Thr Gly Glu Lys Ser Asp Arg Phe Leu  
145 150 155 160

ttc cac tat aac ttc cct ccg tac tct gtc ggt gaa acc ggt cgt atc 528  
Phe His Tyr Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Arg Ile  
165 170 175

ggt tcg ccg aaa cgt cgt gaa atc gcc cac ggt cgt tta gcg aaa cgc 576  
Gly Ser Pro Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg  
180 185 190

ggt gta tta gcg gta atg ccg act gct gaa gaa ttc ccg tat gta gtg 624  
Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val  
195 200 205

gcg gta gta tct gaa att acc gaa tca aac ggt tct tct tca atg gct 672  
Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala  
210 215 220

tcc gta tgc gcc gca tct tta gcg tta atg gac gca gcc gta ccg att 720  
Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile  
225 230 235 240

aaa gcg gcg gtt gcg ggt atc gca atg gcc tta gtg aaa gaa gaa gaa 768  
Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu

245	250	255	
aaa ttt gtg gtg ctt tca gac atc tta ggt gac gaa gac cat tta ggc			816
Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly			
260	265	270	
gat atg gac ttc aaa gta gcc ggt acg cgt gaa ggt gta acc gca ctt			864
Asp Met Asp Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu			
275	280	285	
caa atg gat att aaa atc gaa ggt atc acg cct gaa att atg caa atc			912
Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile			
290	295	300	
gca tta aat caa gcg aaa ggt gcg cgt atg cac atc tta agc gtg atg			960
Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met			
305	310	315	320
gaa caa gcg att cct gca cct cgt gcc gat att tcc gat ttt gcg cct			1008
Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro			
325	330	335	
cgt att cat acg atg aag atc gat ccg aag aaa atc aaa gac gtg atc			1056
Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile			
340	345	350	
ggt aaa ggc ggt gcg gtt at			1076
Gly Lys Gly Gly Ala Val			
355			
<210> 155			
<211> 358			
<212> PRT			
<213> Actinobacillus pleuropneumoniae			
<400> 155			
Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp			
1	5	10	15
Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu			
20	25	30	
Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala			
35	40	45	
Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu			
50	55	60	
Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile			
65	70	75	80
Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu			
85	90	95	
Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile			
100	105	110	
Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg			
115	120	125	
Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp			

130                      135                      140  
 Ala Gln Ile Val Asp Glu Leu Thr Gly Glu Lys Ser Asp Arg Phe Leu  
 145                      150                      155                      160  
 Phe His Tyr Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Arg Ile  
                                  165                      170                      175  
 Gly Ser Pro Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg  
                                  180                      185                      190  
 Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val  
                                  195                      200                      205  
 Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala  
                                  210                      215                      220  
 Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile  
 225                      230                      235                      240  
 Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu  
                                  245                      250                      255  
 Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly  
                                  260                      265                      270  
 Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu  
                                  275                      280                      285  
 Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile  
                                  290                      295                      300  
 Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met  
 305                      310                      315  
 Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro  
                                  325                      330                      335  
 Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile  
                                  340                      345                      350  
 Gly Lys Gly Gly Ala Val  
                                  355

<210> 156  
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 <212> DNA  
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<220>  
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<220>  
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 <222> (1)...(1053)

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 Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala  
   1                                  5                                  10                                  15  
 tta aca gcg tgt aat gaa gaa aag cca aaa gcg gct gaa gca gcg gct 96

Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala	20	25	30	
caa ccg gca gca gcg gga aca gtt cac ctt tat act tgg act gaa tat	144			
Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr	35	40	45	
gtg cct gaa ggc ttg tta gat gaa ttt aca aag caa acc ggt atc aaa	192			
Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys	50	55	60	
gta gag gtt tca agc ctt gaa tct aac gaa acc atg tat gcg aaa tta	240			
Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu	65	70	75	80
aaa tta caa ggt aaa gac ggc ggt tac gat gtt atc gca cct tct aac	288			
Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn	85	90	95	
tac ttc gtt tca aaa atg gcg aaa gaa ggt atg tta gcg gaa tta gat	336			
Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp	100	105	110	
cac gca aaa ctt cct gta atc aaa gag tta aac caa gat tgg tta aac	384			
His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn	115	120	125	
aaa cct tat gac caa ggt aac aaa tac tct tta ccg caa tta tta ggt	432			
Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly	130	135	140	
gca ccg ggt atc gca ttt aac tca aat gac tat aag ggc gat gcg ttc	480			
Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe	145	150	155	160
act tct tgg ggt gat tta tgg aaa cct gag ttt gcg aat aaa gta caa	528			
Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln	165	170	175	
tta tta gat gac gca cgt gaa gta ttt aac att gcg tta tta aaa tta	576			
Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu	180	185	190	
ggt aaa aac cct aat aca acc aat ccg gaa gag att aaa gcg gct tac	624			
Gly Lys Asn Pro Asn Thr Thr Asn Pro Glu Glu Ile Lys Ala Ala Tyr	195	200	205	
gaa gag tta aga aaa tta cgt cca aac gta ctt tct ttc act tca gac	672			
Glu Glu Leu Arg Lys Leu Arg Pro Asn Val Leu Ser Phe Thr Ser Asp	210	215	220	
aac cca gcg aac tca ttt atc gca ggt gaa gta tct gta ggt caa tta	720			
Asn Pro Ala Asn Ser Phe Ile Ala Gly Glu Val Ser Val Gly Gln Leu	225	230	235	240
tgg aac ggt tct gta cgt att gcg aaa aaa gaa caa gcg ccg gta aac	768			
Trp Asn Gly Ser Val Arg Ile Ala Lys Lys Glu Gln Ala Pro Val Asn	245	250	255	
atg gtg ttc cca aaa gaa ggt cct gta ctt tgg gtt gat acg tta gcc	816			
Met Val Phe Pro Lys Glu Gly Pro Val Leu Trp Val Asp Thr Leu Ala				

260	265	270	
att ccg gcg aat gcg aaa aac aaa gaa aat gcg cat aag tta atc aac			864
Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn			
275	280	285	
tac tta tta agc gca ccg gtt gcg gaa aaa tta acg tta gaa atc ggt			912
Tyr Leu Leu Ser Ala Pro Val Ala Glu Lys Leu Thr Leu Glu Ile Gly			
290	295	300	
tat ccg act tca aac gta gaa gcg tta aaa aca tta cca aaa gag att			960
Tyr Pro Thr Ser Asn Val Glu Ala Leu Lys Thr Leu Pro Lys Glu Ile			
305	310	315	320
acc gaa gat ccg gca atc tat ccg aca gct gat gtg tta aaa gcg gca			1008
Thr Glu Asp Pro Ala Ile Tyr Pro Thr Ala Asp Val Leu Lys Ala Ala			
325	330	335	
caa tgg caa gac gat gta ggt aat gca atc gaa ctt tac gaa aaa ta			1055
Gln Trp Gln Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys			
340	345	350	
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Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala			
1	5	10	15
Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala			
20	25	30	
Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr			
35	40	45	
Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys			
50	55	60	
Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu			
65	70	75	80
Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn			
85	90	95	
Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp			
100	105	110	
His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn			
115	120	125	
Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly			
130	135	140	
Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe			
145	150	155	160
Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln			
165	170	175	
Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu			

180	185	190	
Gly Lys Asn Pro Asn Thr Thr	Asn Pro Glu Glu Ile Lys Ala Ala Tyr		
195	200	205	
Glu Glu Leu Arg Lys Leu Arg Pro Asn Val Leu Ser Phe Thr Ser Asp			
210	215	220	
Asn Pro Ala Asn Ser Phe Ile Ala Gly Glu Val Ser Val Gly Gln Leu			
225	230	235	240
Trp Asn Gly Ser Val Arg Ile Ala Lys Lys Glu Gln Ala Pro Val Asn			
245	250	255	
Met Val Phe Pro Lys Glu Gly Pro Val Leu Trp Val Asp Thr Leu Ala			
260	265	270	
Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn			
275	280	285	
Tyr Leu Leu Ser Ala Pro Val Ala Glu Lys Leu Thr Leu Glu Ile Gly			
290	295	300	
Tyr Pro Thr Ser Asn Val Glu Ala Leu Lys Thr Leu Pro Lys Glu Ile			
305	310	315	320
Thr Glu Asp Pro Ala Ile Tyr Pro Thr Ala Asp Val Leu Lys Ala Ala			
325	330	335	
Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys			
340	345	350	

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 <211> 525  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae  
 <220>  
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 Met Gln Lys Val Lys Leu Pro Leu Thr Ile Asp Pro Tyr Lys Asp Ala  
 1 5 10 15  
 cag cgt cga atg gat tac gaa ggc tac atc tca cgt agt ctg ctt aat 96  
 Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Asn  
 20 25 30  
 cgt ttg ggt gaa tct gtg agc aat gtg cta agc gat gca caa gtt act 144  
 Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr  
 35 40 45  
 ctc tcg tta tat atc gat ccg caa cgc tta acc gtt att aaa ggt acg 192  
 Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr  
 50 55 60  
 gcg aca gtg gaa gtg gaa ttc gat tgc caa cga tgc ggt aac ccg ttt 240

Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe  
65 70 80

aca caa acg ctt gac tgt tgc ttt tgt ttc agt ccg gtg tcc aat atg 288  
Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met  
85 90 95

gat cag gcg gac aat ttg ccc gaa att tat gaa cca atc gaa gta aac 336  
Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn  
100 105 110

gag ttc ggt gaa gta aat tta cta gat atg atc gaa gat gga ttt atc 384  
Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile  
115 120 125

atc gaa ttg cct cta gtc ccg atg cat agt gaa gaa cac tgt gaa gtg 432  
Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val  
130 135 140

tcc gtg agt gaa cag gtg ttt ggc gaa ttg cct gaa gaa ttg gcg aaa 480  
Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys  
145 150 155 160

aaa cct aac ccg ttc gct gta tta gct aat tta aag aaa aac tag 525  
Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn  
165 170

<210> 159  
<211> 174  
<212> PRT  
<213> Actinobacillus pleuropneumoniae

<400> 159  
Met Gln Lys Val Lys Leu Pro Leu Thr Ile Asp Pro Tyr Lys Asp Ala  
1 5 10 15

Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn  
20 25 30

Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr  
35 40 45

Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr  
50 55 60

Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe  
65 70 75 80

Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met  
85 90 95

Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn  
100 105 110

Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile  
115 120 125

Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val  
130 135 140

Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys  
145 150 155 160

Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn  
 165 170

<210> 160

<211> 1302

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> tig

<220>

<221> CDS

<222> (1)..(1299)

<400> 160

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 Met Ser Ile Ser Ile Glu Thr Leu Glu Gly Leu Gln Arg Arg Val Thr  
 1 5 10 15

att acc gta gct gct gat aaa atc gaa gcg gct tac aaa gag caa tta 96  
 Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu  
 20 25 30

aaa ggc tat gcg aaa aac gct cgt gta gac ggt ttc cgt aaa ggt aaa 144  
 Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys  
 35 40 45

gta ccg cac gca att atc gaa caa cgt ttc ggt tta gcg gct cgc caa 192  
 Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln  
 50 55 60

gac gta tta tcc gat gaa atg caa cgt gcg ttc ttt gat gcg gta atc 240  
 Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile  
 65 70 75 80

gct gag aaa att aac ctt gcc ggt cgt cct acc ttc aca ccg aac aac 288  
 Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn  
 85 90 95

tac caa ccg agt caa gaa ttc agc ttc act gca act ttt gaa gta ttc 336  
 Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe  
 100 105 110

ccg gaa gtt gaa tta aaa ggc tta gaa aat atc gaa gtt gaa aaa ccg 384  
 Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro  
 115 120 125

gtt gta gaa atc aca gaa gct gat tta gac aaa atg atc gat gtg tta 432  
 Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu  
 130 135 140

cgt aaa caa caa gcg act tgg gct gaa tct caa gca gcg gca caa gcg 480  
 Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala  
 145 150 155 160

gaa gac cgt gtt gta atc gac ttc gta ggt tct gta gac ggt gaa gag 528  
 Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu  
 165 170 175

ttt gaa ggc ggt aaa gcg aca gac ttc act tta gca atg ggt caa agt 576  
 Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser

180	185	190	
cgt atg atc cct ggt ttt gaa gaa ggt atc gtt ggt cac aaa gcc ggc 624			
Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly			
195	200	205	
gaa caa ttc gat atc gat gtt act ttc cct gaa gaa tac cac gct gaa 672			
Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu			
210	215	220	
aac tta aaa ggt aaa gcg gcg aaa ttc gca att aca ctt aag aaa gta 720			
Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val			
225	230	235	240
gaa aat atc gta tta cct gaa tta acc gaa gaa ttc gtg aaa aaa ttc 768			
Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe			
	245	250	255
ggt tca gca aaa act gta gaa gat tta cgt gcg gaa att aag aaa aat 816			
Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn			
	260	265	270
atg caa cgt gaa ctt aaa aac gca gta acc gca gcg gtt aaa aac caa 864			
Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln			
	275	280	285
gta atc aac ggt tta atc gca caa aat gaa att gaa gtg ccg gct gca 912			
Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala			
	290	295	300
gcg gta gcg gaa gaa gtg gac gta tta cgt cgt caa gcg gtt caa cgt 960			
Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg			
305	310	315	320
ttc ggt ggt aaa ccg gaa atg gct gca caa tta ccg gcg gaa tta ttc 1008			
Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe			
	325	330	335
gaa gcg gat gca aaa cgt cgt gtt caa gta ggt tta tta ctt tca acc 1056			
Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Ser Thr			
	340	345	350
gta atc ggt act aac gaa tta aaa gtt gat gaa aaa cgt gtt gaa gaa 1104			
Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu			
	355	360	365
acg att gca gaa atc gct tca gct tac gaa caa ccg gcg gaa gtt gtt 1152			
Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val			
	370	375	380
gct cat tat gcg aaa aac cgt caa tta acc gaa aat atc cgt aac gta 1200			
Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val			
385	390	395	400
gtg tta gaa gag caa gcg gtt gaa gtt gta ctt gcg aaa gca aaa gta 1248			
Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val			
	405	410	415
act gaa aaa gcg act tct ttt gat gaa gta atg gct caa caa gct caa 1296			
Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln			
	420	425	430
ggc taa			1302

Gly

&lt;210&gt; 161

&lt;211&gt; 433

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 161

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Met Ser Ile Ser Ile Glu Thr Leu Glu Gly Leu Gln Arg Arg Val Thr
 1           5           10           15

Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu
          20           25           30

Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys
          35           40           45

Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln
          50           55           60

Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile
          65           70           75           80

Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn
          85           90           95

Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe
          100          105          110

Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro
          115          120

Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu
          130          135          140

Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala
          145          150          155          160

Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu
          165          170          175

Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser
          180          185          190

Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly
          195          200          205

Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu
          210          215          220

Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val
          225          230          235          240

Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe
          245          250          255

Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn
          260          265          270

Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln
          275          280          285

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Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala
 290                295                300
Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg
 305                310                315                320
Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe
                325                330                335
Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr
                340                345                350
Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu
 355                360                365
Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val
 370                375                380
Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val
 385                390                395                400
Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val
                405                410                415
Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln
 420                425                430

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Gly

&lt;210&gt; 162

&lt;211&gt; 316

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; tRNA-glu

&lt;400&gt; 162

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aatattgcgc tcaaatggca aagcggagag catctttaaa tgttgtcccc atcgcttaga 60
ggcctaggac atcgcccttt cacggcggtta accgggggttc gaatccccgt ggggaagcca 120
tttaaagatg acttttggtg tctgaattgt tctttaaaaa attggaaaca agctgaaaaa 180
tgagagattt tcgaaagaaa gtctgagtag taaaagataa gtaattatct tgaaaatctt 240
agctgaacaa aagcagctaa gtgtttagtt gaataaagta tcgcgttgaa tgcgttcaaa 300
taaaatttga aaatat
                                     316

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&lt;210&gt; 163

&lt;211&gt; 85

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; tRNA-leu

&lt;400&gt; 163

```

gctctgggtg tggaattggt agacacgcta tcttgagggg gtagtgtcca taggatgtgc 60

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gagttcagat ctcgccaga gcacc

85

&lt;210&gt; 164

&lt;211&gt; 623

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; yaeE

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (621)

&lt;400&gt; 164

atg	caa	gaa	ctc	aca	cct	caa	atg	tgg	ggc	tta	gtc	ggc	act	tca	acg	48
Met	Gln	Glu	Leu	Thr	Pro	Gln	Met	Trp	Gly	Leu	Val	Gly	Thr	Ser	Thr	
1					5				10					15		

ctt	gaa	acg	ctc	tat	atg	ggc	ttt	gcg	gcg	act	tta	ctt	gct	gtg	gta	96
Leu	Glu	Thr	Leu	Tyr	Met	Gly	Phe	Ala	Ala	Thr	Leu	Leu	Ala	Val	Val	
			20					25					30			

gtc	ggt	ttg	ccg	atc	ggt	ttt	ctg	gca	ttt	tta	acc	ggt	aaa	gga	gag	144
Val	Gly	Leu	Pro	Ile	Gly	Phe	Leu	Ala	Phe	Leu	Thr	Gly	Lys	Gly	Glu	
		35					40					45				

att	tta	gag	aat	ccg	cgt	tta	cat	caa	gta	tta	gat	gtg	att	att	aat	192
Ile	Leu	Glu	Asn	Pro	Arg	Leu	His	Gln	Val	Leu	Asp	Val	Ile	Ile	Asn	
		50				55					60					

atc	ggt	cgt	tcc	gta	ccg	ttt	att	att	ttg	tta	gtc	gtg	ttg	tta	cct	240
Ile	Gly	Arg	Ser	Val	Pro	Phe	Ile	Ile	Leu	Val	Val	Val	Leu	Leu	Pro	
		65			70					75					80	

ttt	acg	cgt	tta	ttg	gtc	ggg	aca	acg	ctc	ggt	act	acg	gcg	gcg	att	288
Phe	Thr	Arg	Leu	Leu	Val	Gly	Thr	Thr	Leu	Gly	Thr	Thr	Ala	Ala	Ile	
			85						90					95		

gtg	ccg	tta	agc	ggt	tcg	gca	att	ccg	ttt	ttt	gcg	cgt	tta	act	tca	336
Val	Pro	Leu	Ser	Val	Ser	Ala	Ile	Pro	Phe	Phe	Ala	Arg	Leu	Thr	Ser	
		100						105					110			

aat	gcg	tta	tta	gaa	atc	cca	gca	ggt	tta	acc	gaa	gcg	gcg	aaa	tcg	384
Asn	Ala	Leu	Leu	Glu	Ile	Pro	Ala	Gly	Leu	Thr	Glu	Ala	Lys	Ser		
		115					120					125				

atg	ggc	gca	acg	aat	tgg	caa	gtg	gtc	agt	aaa	ttt	tat	tta	ccg	gaa	432
Met	Gly	Ala	Thr	Asn	Trp	Gln	Val	Val	Ser	Lys	Phe	Tyr	Leu	Pro	Glu	
		130				135					140					

tca	ctg	ccg	att	tta	atc	aat	ggt	atc	aca	tta	act	tta	gtc	gct	tta	480
Ser	Leu	Pro	Ile	Leu	Ile	Asn	Gly	Ile	Thr	Leu	Thr	Leu	Val	Ala	Leu	
		145				150				155				160		

atc	ggt	tat	tcg	gca	atg	gcg	ggt	gcg	gtc	ggc	ggc	ggc	ggt	ttg	ggg	528
Ile	Gly	Tyr	Ser	Ala	Met	Ala	Gly	Ala	Val	Gly	Gly	Gly	Gly	Leu	Gly	
			165					170						175		

aac	ctt	gcc	atc	agt	tac	ggt	gaa	cac	cga	aat	atg	gtc	tat	gta	aaa	576
Asn	Leu	Ala	Ile	Ser	Tyr	Gly	Glu	His	Arg	Asn	Met	Val	Tyr	Val	Lys	
			180					185						190		

tgg atc tca aca att att atc gta gcg att gtg atg atc agt caa aa 623  
 Trp Ile Ser Thr Ile Ile Ile Val Ala Ile Val Met Ile Ser Gln  
 195 200 205

<210> 165  
 <211> 207  
 <212> PRT  
 <213> *Actinobacillus pleuropneumoniae*

<400> 165  
 Met Gln Glu Leu Thr Pro Gln Met Trp Gly Leu Val Gly Thr Ser Thr  
 1 5 10 15  
 Leu Glu Thr Leu Tyr Met Gly Phe Ala Thr Leu Leu Ala Val Val  
 20 25 30  
 Val Gly Leu Pro Ile Gly Phe Leu Ala Phe Leu Thr Gly Lys Gly Glu  
 35 40 45  
 Ile Leu Glu Asn Pro Arg Leu His Gln Val Leu Asp Val Ile Ile Asn  
 50 55 60  
 Ile Gly Arg Ser Val Pro Phe Ile Ile Leu Leu Val Val Leu Leu Pro  
 65 70 75 80  
 Phe Thr Arg Leu Leu Val Gly Thr Thr Leu Gly Thr Thr Ala Ala Ile  
 85 90 95  
 Val Pro Leu Ser Val Ser Ala Ile Pro Phe Phe Ala Arg Leu Thr Ser  
 100 105 110  
 Asn Ala Leu Leu Glu Ile Pro Ala Gly Leu Thr Glu Ala Lys Ser  
 115 120 125  
 Met Gly Ala Thr Asn Trp Gln Val Val Ser Lys Phe Tyr Leu Pro Glu  
 130 135 140  
 Ser Leu Pro Ile Leu Ile Asn Gly Ile Thr Leu Thr Leu Val Ala Leu  
 145 150 155 160  
 Ile Gly Tyr Ser Ala Met Ala Gly Ala Val Gly Gly Gly Leu Gly  
 165 170 175  
 Asn Leu Ala Ile Ser Tyr Gly Glu His Arg Asn Met Val Tyr Val Lys  
 180 185 190  
 Trp Ile Ser Thr Ile Ile Ile Val Ala Ile Val Met Ile Ser Gln  
 195 200 205

<210> 166  
 <211> 866  
 <212> DNA  
 <213> *Pasteurella (Mannheimia) haemolytica*

<220>  
 <221> CDS  
 <222> (1)..(864)  
 <220>  
 <223> atpG

<400> 166  
 atg gca ggt gct aaa gag ata aga acc aaa att gca agt gtt cgt aat 48  
 Met Ala Gly Ala Lys 5 Glu Ile Arg Thr Lys 10 Ile Ala Ser Val Arg Asn 15  
 1

aca caa aaa att acc aaa gcg atg gaa atg gtt gcc gca tca aaa atg 96  
 Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys Met 20 25 30

cgt aaa acc caa gag cgt atg gcg gct tct cgc cct tat gct gaa agt 144  
 Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ala Glu Ser 35 40 45

att cgc aag gca att agc cat att gcc aaa ggt aac att gag tat aaa 192  
 Ile Arg Lys Ala Ile Ser His 55 Ile Ala Lys Gly Asn 60 Ile Glu Tyr Lys 50

cac cca ttt ttg acc cca cgt ccg gta aaa aaa gtt gcc tat tta gta 240  
 His Pro Phe Leu Thr Pro Arg Pro Val Lys Lys Val Gly Tyr Leu Val 65 70 75 80

gtt tca acc gat cgc ggt tta tgt ggt gcc tta aat atc aat tta ttt 288  
 Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe 85 90 95

aaa acc gtt tta cat gaa ttg aaa gaa aaa gat gac caa ggt gtt aag 336  
 Lys Thr Val Leu His Glu Leu Lys Glu Lys Asp Asp Gln Gly Val Lys 100 105 110

tct cga ctt gct gtg gtg gga aat aaa ggg atc tcc ttt ttt aac cca 384  
 Ser Arg Leu Ala Val Val Gly Asn Lys Lys Gly Ile Ser Phe Phe Asn Pro 115 120 125

atg ggg cta gag att aaa ggt cat atc aat gga ttg ggt gat aca ccg 432  
 Met Gly Leu Glu Ile Lys Gly His Ile Asn Gly Leu Gly Asp Thr Pro 130 135 140

gca atg gaa gat tta gtc ggt att gtt aat ggt atg gta aat gcc tac 480  
 Ala Met Glu Asp Leu Val Gly Ile Val Asn Gly Met Val Asn Ala Tyr 145 150 155 160

cgt gaa ggc gaa att gat gaa gtg tat gtg gta tat aac cgt ttt ata 528  
 Arg Glu Gly Glu Ile Asp Glu Val Tyr Val Val Tyr Asn Arg Phe Ile 165 170 175

aac acg atg tca caa aaa ccg aca gta caa cag ttg ctt cct ttg cct 576  
 Asn Thr Met Ser Gln Lys Pro Thr Val Gln Gln Leu Leu Pro Leu Pro 180 185 190

gca ctg gaa aat gac tca tta gag caa act ggt tct tgg gat tat ctc 624  
 Ala Leu Glu Asn Asp Ser Leu Glu Gln Thr Gly Ser Txp Asp Tyr Leu 195 200 205

tat gaa cca aat cca caa gcg tta tta gac agc tta ctg gtt cgt tat 672  
 Tyr Glu Pro Asn Pro Gln Ala Leu Leu Asp Ser Leu Leu Val Arg Tyr 210 215 220

tta gaa tct caa gtt tat cag gca gtg gta gat aat ctt gcg tct gaa 720  
 Leu Glu Ser Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu 225 230 235 240

cag gct gct cga atg gtg gca atg aaa gca gca acc gat aac gca ggt 768  
 Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly

	245	250	255	
aat ctg att	aat gag tta	cag tta gtg	tat aac aaa gct	cgt caa gca 816
Asn Leu Ile	Asn Glu Leu	Gln Leu Val	Tyr Asn Lys Ala	Arg Gln Ala
	260	265	270	
agt att acg	aat gaa tta	aat gaa att	gtc gcg ggt gcc	gca gca att 864
Ser Ile Thr	Asn Glu Leu	Asn Glu Ile	Val Ala Gly Ala	Ala Ala Ile
	275	280	285	
ta				866
<210> 167				
<211> 288				
<212> PRT				
<213> Pasteurella (Mannheimia) haemolytica				
<400> 167				
Met Ala Gly	Ala Lys Glu	Ile Arg Thr	Lys Ile Ala	Ser Val Arg Asn
1	5	10	15	
Thr Gln Lys	Ile Thr Lys	Ala Met Glu	Met Val Ala	Ala Ser Lys Met
	20	25	30	
Arg Lys Thr	Gln Glu Arg	Met Ala Ala	Ser Arg Pro	Tyr Ala Glu Ser
	35	40	45	
Ile Arg Lys	Ala Ile Ser	His Ile Ala	Lys Gly Asn	Ile Glu Tyr Lys
	50	55	60	
His Pro Phe	Leu Thr Pro	Arg Pro Val	Lys Lys Val	Gly Tyr Leu Val
	65	70	75	80
Val Ser Thr	Asp Arg Gly	Leu Cys Gly	Gly Leu Asn	Ile Asn Leu Phe
	85	90	95	
Lys Thr Val	Leu His Glu	Leu Lys Glu	Lys Asp Asp	Gln Gly Val Lys
	100	105	110	
Ser Arg Leu	Ala Val Val	Gly Asn Lys	Gly Ile Ser	Phe Phe Asn Pro
	115	120	125	
Met Gly Leu	Glu Ile Lys	Gly His Ile	Asn Gly Leu	Gly Asp Thr Pro
	130	135	140	
Ala Met Glu	Asp Leu Val	Gly Ile Val	Asn Gly Met	Val Asn Ala Tyr
	145	150	155	160
Arg Glu Gly	Glu Ile Asp	Glu Val Tyr	Val Val Tyr	Asn Arg Phe Ile
	165	170	175	
Asn Thr Met	Ser Gln Lys	Pro Thr Val	Gln Gln Leu	Leu Pro Leu Pro
	180	185	190	
Ala Leu Glu	Asn Asp Ser	Leu Glu Gln	Thr Gly Ser	Trp Asp Tyr Leu
	195	200	205	
Tyr Glu Pro	Asn Pro Gln	Ala Leu Leu	Asp Ser Leu	Leu Val Arg Tyr
	210	215	220	
Leu Glu Ser	Gln Val Tyr	Gln Ala Val	Val Asp Asn	Leu Ala Ser Glu
	225	230	235	240

Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly  
 245 250 255

Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala  
 260 265 270

Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile  
 275 280 285

<210> 168

<211> 1463

<212> DNA

<213> Pasteurella (Mannheimia) haemolytica

<220>

<221> CDS

<222> (1)..(1461)

<220>

<223> guaB

<400> 168

atg cta cga att aaa caa gaa gcc ctc act ttt gat gat gtt ctt ctc 48  
 Met Leu Arg Ile Lys Gln Glu Ala Leu Thr Phe Asp Asp Val Leu Leu  
 1 5 10 15

gtc ccg gca cat tct act gtg ctt cct aat act gct gat ctt tct act 96  
 Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr  
 20 25 30

caa tta act aaa acc att cgt tta aac att ccg atg ctt tct gct gca 144  
 Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala  
 35 40 45

atg gat acc gtt aca gaa act aag ctt gcg atc tcc ctt gct caa gaa 192  
 Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu  
 50 55 60

ggc ggc att ggt ttt atc cat aaa aat atg tcg att gaa cgc cag gca 240  
 Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala  
 65 70 75 80

gac cgt gtg cgt aaa gtg aaa aaa ttt gaa agt ggt att gtt tct gag 288  
 Asp Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Glu  
 85 90 95

cca gtg acg att tct cct gat atg aca tta gcg gaa ttg gct gaa ttg 336  
 Pro Val Thr Ile Ser Pro Asp Met Thr Leu Ala Glu Leu Ala Glu Leu  
 100 105 110

gtg aaa aag aac ggt ttt gca gcc tat ccg gtg att gat gaa aac caa 384  
 Val Lys Lys Asn Gly Phe Ala Gly Tyr Pro Val Ile Asp Glu Asn Gln  
 115 120 125

aat tta gtg gga att att acc gga cgt gat acc cga ttt gtc acg gat 432  
 Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp  
 130 135 140

tta agc aaa aca gtg cgt gaa ttt atg aca cca aaa gac cgt tta gtg 480  
 Leu Ser Lys Thr Val Arg Glu Phe Met Thr Pro Lys Asp Arg Leu Val  
 145 150 155 160

acg gta aaa gaa aac gca agc cgt gaa gaa att ttc cac tta atg cac	528
Thr Val Lys Glu Asn Ala Ser Arg Glu Glu Ile Phe His Leu Met His	
165 170 175	
gaa cac cga gtg gag aaa gtg ctg gta gtg aat aat gaa ttt cag tta	576
Glu His Arg Val Glu Lys Val Leu Val Val Asn Asn Glu Phe Gln Leu	
180 185 190	
aaa gga atg att acc cta aaa gac tac caa aaa gcg gaa agc aaa ccg	624
Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ala Glu Ser Lys Pro	
195 200 205	
aat gcc tgt aaa gat gag ttt ggg cgt ttg cgt gtg ggg gcg gca gtg	672
Asn Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val	
210 215 220	
gga gcc ggt ccg ggc aat gaa gaa cga att gat gct tta gta aaa gcg	720
Gly Ala Gly Pro Glu Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala	
225 230 235 240	
ggg gtc gat gtg cta tta atc gac tct tcg cac ggg cat tct gaa ggt	768
Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly	
245 250 255	
gta tta caa cgt gtg cgt gaa acc cgt gca aaa tac cct gat tta ccg	816
Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro	
260 265 270	
att gtt gcc ggt aat att gcc act gca gaa gga gcg att gcg tta gct	864
Ile Val Ala Gly Asn Ile Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala	
275 280 285	
gat gca gga gcc agt gct gtg aaa gta gga atc ggc ccg ggt tca att	912
Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile	
290 295 300	
tgt acc acc aga att gta aca ggc gtt ggc gtg cca caa atc acg gca	960
Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala	
305 310 315 320	
atc gca gaa gcg gca gct gcg ctt aaa gaa cga ggc att cct gtg att	1008
Ile Ala Glu Ala Ala Ala Leu Lys Glu Arg Gly Ile Pro Val Ile	
325 330 335	
gct gat ggt gga att cgt tat tca ggc gat att tca aaa gct att gcc	1056
Ala Asp Gly Gly Ile Arg Tyr Ser Gly Asp Ile Ser Lys Ala Ile Ala	
340 345 350	
gcc ggt gca agt tgc gta atg gtc ggt tcg atg ttt gcc ggc aca gaa	1104
Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu	
355 360 365	
gaa gcc ccg ggt gaa att gag ctt tat caa ggc aga gca ttc aaa tcc	1152
Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser	
370 375 380	
tac cgt gga atg gga tca tta ggt gca atg agt aaa ggc tcg tca gat	1200
Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Lys Gly Ser Ser Asp	
385 390 395 400	
gcg tat ttc caa tct gat aat gcc gcc gac aag ctc gta ccg gaa ggg	1248
Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly	
405 410 415	

att gaa ggg cgt atc gct tac aaa ggc tac ttg aaa gaa att atc cac 1296  
 Ile Glu Gly Arg Ile Ala Tyr Lys Gly Tyr Leu Lys Glu Ile Ile His  
 420 425 430

caa caa atg ggc ggc tta cgc tcc tgt atg gga tta acc ggc tgt gcc 1344  
 Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala  
 435 440 445

act att gaa gaa ctc cgc acc aaa gca gaa ttt gtc cgc att agt ggt 1392  
 Thr Ile Glu Glu Leu Arg Thr Lys Ala Glu Phe Val Arg Ile Ser Gly  
 450 455 460

gct ggt att aaa gaa agc cac gtc cac gat gtg aca att acc aaa gaa 1440  
 Ala Gly Ile Lys Glu Ser His Val His Asp Val Thr Ile Thr Lys Glu  
 465 470 475 480

gca ccg aac tac cga atg ggt ta 1463  
 Ala Pro Asn Tyr Arg Met Gly  
 485

&lt;210&gt; 169

&lt;211&gt; 487

&lt;212&gt; PRT

&lt;213&gt; Pasteurella (Mannheimia) haemolytica

&lt;400&gt; 169

Met Leu Arg Ile Lys Gln Glu Ala Leu Thr Phe Asp Asp Val Leu Leu  
 1 5 10 15

Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr  
 20 25 30

Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala  
 35 40 45

Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu  
 50 55 60

Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala  
 65 70 75 80

Asp Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Glu  
 85 90 95

Pro Val Thr Ile Ser Pro Asp Met Thr Leu Ala Glu Leu Ala Glu Leu  
 100 105 110

Val Lys Lys Asn Gly Phe Ala Gly Tyr Pro Val Ile Asp Glu Asn Gln  
 115 120 125

Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp  
 130 135 140

Leu Ser Lys Thr Val Arg Glu Phe Met Thr Pro Lys Asp Arg Leu Val  
 145 150 155 160

Thr Val Lys Glu Asn Ala Ser Arg Glu Glu Ile Phe His Leu Met His  
 165 170 175

Glu His Arg Val Glu Lys Val Leu Val Val Asn Asn Glu Phe Gln Leu  
 180 185 190

Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ala Glu Ser Lys Pro  
 195 200 205  
 Asn Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val  
 210 215 220  
 Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala  
 225 230 235 240  
 Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly  
 245 250 255  
 Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro  
 260 265 270  
 Ile Val Ala Gly Asn Ile Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala  
 275 280 285  
 Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile  
 290 295 300  
 Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala  
 305 310 315 320  
 Ile Ala Glu Ala Ala Ala Leu Lys Glu Arg Gly Ile Pro Val Ile  
 325 330 335  
 Ala Asp Gly Gly Ile Arg Tyr Ser Gly Asp Ile Ser Lys Ala Ile Ala  
 340 345 350  
 Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu  
 355 360 365  
 Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser  
 370 375 380  
 Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp  
 385 390 395 400  
 Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly  
 405 410 415  
 Ile Glu Gly Arg Ile Ala Tyr Lys Gly Tyr Leu Lys Glu Ile Ile His  
 420 425 430  
 Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala  
 435 440 445  
 Thr Ile Glu Glu Leu Arg Thr Lys Ala Glu Phe Val Arg Ile Ser Gly  
 450 455 460  
 Ala Gly Ile Lys Glu Ser His Val His Asp Val Thr Ile Thr Lys Glu  
 465 470 475 480  
 Ala Pro Asn Tyr Arg Met Gly  
 485

&lt;210&gt; 170

&lt;211&gt; 2150

&lt;212&gt; DNA

&lt;213&gt; Pasteurella (Mannheimia) haemolytica

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (2148)

&lt;220&gt;

&lt;223&gt; pnp

&lt;400&gt; 170

atg act cca att gta aaa cag ttt aaa tac ggt cag cac acc gtg acc	48
Met Thr Pro Ile Val Lys Gln Phe Lys Tyr Gln His Thr Val Thr	
1 5 10 15	
tta gaa acc ggt gct atc gca cgc caa gca acg gca gca gta atg gca	96
Leu Glu Thr Gly Ala Ile Ala Arg Gln Ala Thr Ala Val Met Ala	
20 25 30	
agt atg gac gac aca acc gta ttt gtt acc gta gta gcg aaa aaa gac	144
Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys Lys Asp	
35 40 45	
gta aaa gaa ggg caa gat ttc ttc cca tta acc gta gat tat caa gag	192
Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asp Tyr Gln Glu	
50 55 60	
cgt act tac gca gcc ggt cgt att ccg ggc ggt ttc ttc aaa cgt gaa	240
Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Phe Phe Lys Arg Glu	
65 70 75 80	
gga cgt cct agc gaa ggt gaa acc tta atc gct cgc ttg atc gac cgt	288
Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile Asp Arg	
85 90 95	
cct gtg cgt cca ctt ttc cca gaa ggt ttc ttt aac gaa att caa gtg	336
Pro Val Arg Pro Leu Phe Pro Glu Gly Phe Phe Asn Glu Ile Gln Val	
100 105 110	
att gcg acc gta gta tcg gta aac cca caa atc agt cct gat ctg gtt	384
Ile Ala Thr Val Val Ser Val Asn Pro Gln Ile Ser Pro Asp Leu Val	
115 120 125	
gcg atg atc ggt gca tcg gct gcc ctt tca tta tcc ggc gtg ccg ttt	432
Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val Pro Phe	
130 135 140	
aac ggt cca atc ggt gcg gct cgt gtc ggt ttt atc aac gat caa ttc	480
Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asn Asp Gln Phe	
145 150 155 160	
gta tta aac cca acc acc agc gag caa aaa atc agc cgc tta gat tta	528
Val Leu Asn Pro Thr Thr Ser Glu Gln Lys Ile Ser Arg Leu Asp Leu	
165 170 175	
gtg gtt tca ggt aca gac aaa gcc gtg ttg atg gtg gaa tct gaa gcg	576
Val Val Ser Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser Glu Ala	
180 185 190	
gat atc tta acc gaa gag caa atg tta gcg gcg gtg gtg ttc ggc cac	624
Asp Ile Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe Gly His	
195 200 205	
gag caa caa cag gtt gta atc gaa aac atc aaa gaa ttt gtt aaa gaa	672
Glu Gln Gln Gln Val Val Ile Glu Asn Ile Lys Glu Phe Val Lys Glu	
210 215 220	

gcg ggc aaa cca cgt tgg gat tgg gtt gca cca gag cca aat aca gat Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn Thr Asp 225 230 235 240	720
tta atc aac aaa gta aaa gca tta gca gaa aca cgc ctt ggc gat gct Leu Ile Asn Lys Val Lys Ala Leu Ala Glu Thr Arg Leu Gly Asp Ala 245 250 255	768
tat cgt atc gta gaa aaa caa gtt cgt tac gag caa atc gat gcg att Tyr Arg Ile Val Glu Lys Gln Val Arg Tyr Glu Gln Ile Asp Ala Ile 260 265 270	816
aaa gca gag gtg att gca caa ctt acc gca gaa gat gaa act gtt tct Lys Ala Glu Val Ile Ala Gln Leu Thr Ala Glu Asp Glu Thr Val Ser 275 280 285	864
gaa ggg act atc atc gac atc atc acc gca tta gag agc caa atc gtg Glu Gly Thr Ile Ile Asp Ile Ile Thr Ala Leu Glu Ser Gln Ile Val 290 295 300	912
cgt agc cgt att att gca ggc gaa cca cgc att gac ggc cgt acg gtg Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr Val 305 310 315 320	960
gat acc gtg cgt gca ttg gat att tgc acc agt gtg tta cca cgc acc Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Ser Val Leu Pro Arg Thr 325 330 335	1008
cac ggt tct gct ctt ttc acc cgt ggc gaa acc caa gca tta gca gta His Gly Ser Ala Leu Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala Val 340 345 350	1056
gca aca ttg ggc aca gag cgt gat gcc caa atc att gac gaa ttg acc Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu Thr 355 360 365	1104
ggc gaa aaa tct gac cgt ttc tta ttc cac tac aat ttc cct cca tac Gly Glu Lys Ser Asp Arg Phe Leu Phe His Tyr Asn Phe Pro Pro Tyr 370 375 380	1152
tct gtg ggc gaa acc ggt cgt atc ggc tcg cca aaa cgc cgt gaa atc Ser Val Gly Glu Thr Gly Arg Ile Gly Ser Pro Lys Arg Arg Glu Ile 385 390 395 400	1200
ggt cac ggt cgt tta gca aaa cgt ggc gta tta gcc gtg atg cca acc Gly His Gly Arg Leu Ala Lys Arg Gly Val Leu Ala Val Met Pro Thr 405 410 415	1248
gct gaa gag ttc ccg tat gta gtg cgt gtg gtg tct gaa atc act gaa Ala Glu Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr Glu 420 425 430	1296
tct aac ggt tct tct tca atg gca tct gtg tgt ggt gcg tct ctt gcg Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu Ala 435 440 445	1344
ttg atg gac gca ggt gtg cca atc aaa gca gcg gtt gcc ggt atc gca Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile Ala 450 455 460	1392
atg ggg ctc gtg aaa gaa gac gag aaa ttc gtg gta ctt tct gac atc Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp Ile 465 470 475 480	1440

tta ggt gat gaa gac cac tta ggc gat atg gac ttt aaa gta gcg gga	1488
Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala Gly	
485 490 495	
acc cgt acc ggt gtg act gcg ctg caa atg gac atc aaa atc gaa ggg	1536
Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu Gly	
500 505 510	
atc acc cct gaa att atg cgt att gcc tta aac caa gct aaa ggt gca	1584
Ile Thr Pro Glu Ile Met Arg Ile Ala Leu Asn Ala Lys Gly Ala	
515 520 525	
aga atg cac att tta ggt gta atg gaa caa gcc att ccg gca cct cgt	1632
Arg Met His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro Arg	
530 535 540	
gca gat att tct gac tat gcc cca cgc att cac aca atg aag atc gat	1680
Ala Asp Ile Ser Asp Tyr Ala Pro Arg Ile His Thr Met Lys Ile Asp	
545 550 555 560	
ccg aag aaa atc aaa gat gtg att ggt aaa ggc ggt gca aca att cgt	1728
Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Ala Thr Ile Arg	
565 570 575	
gct tta acc gaa gag acc aat act tct atc gac att gat gat gac ggt	1776
Ala Leu Thr Glu Glu Thr Asn Thr Ser Ile Asp Ile Asp Asp Gly	
580 585 590	
acg gtg aaa att gcg gca act gac ggc aat gca gcg aaa gca gta atg	1824
Thr Val Lys Ile Ala Ala Thr Asp Gly Asn Ala Ala Lys Ala Val Met	
595 600 605	
gct cgt att gaa gag atc gtt gcc gaa gtg gaa gta aac caa atc tac	1872
Ala Arg Ile Glu Glu Ile Val Ala Glu Val Glu Val Asn Gln Ile Tyr	
610 615 620	
aac ggt aaa gta acc cgt gtg gtg gac ttc ggt gca ttc gtt tcc atc	1920
Asn Gly Lys Val Thr Arg Val Val Asp Phe Gly Ala Phe Val Ser Ile	
625 630 635 640	
tta ggt ggc aaa gaa ggt tta gtc cac att tca caa atc acc aac gaa	1968
Leu Gly Gly Lys Glu Gly Leu Val His Ile Ser Gln Ile Thr Asn Glu	
645 650 655	
cgt gtt gag cgt gta gcg gac tac tta acc gtt ggt caa gaa gta caa	2016
Arg Val Glu Arg Val Ala Asp Tyr Leu Thr Val Gly Gln Glu Val Gln	
660 665 670	
gtg aaa gtg gta gaa att gac cgt caa gga cgc att cgt ctg acg atg	2064
Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr Met	
675 680 685	
aaa gac atc aat aat acc aac gag gca aat gca gaa gaa act gta gct	2112
Lys Asp Ile Asn Asn Thr Asn Glu Ala Asn Ala Glu Glu Thr Val Ala	
690 695 700	
gaa aat gtg gta gaa aca gaa caa gaa aat aat ttc ta	2150
Glu Asn Val Val Glu Thr Glu Gln Glu Asn Asn Phe	
705 710 715	

&lt;210&gt; 171

&lt;211&gt; 716

&lt;212&gt; PRT

<213> *Pasteurella (Mannheimia) haemolytica*

&lt;400&gt; 171

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Met Thr Pro Ile Val Lys Gln Phe Lys Tyr Gly Gln His Thr Val Thr
 1              5              10              15

Leu Glu Thr Gly Ala Ile Ala Arg Gln Ala Thr Ala Ala Val Met Ala
      20              25              30

Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys Lys Asp
      35              40              45

Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asp Tyr Gln Glu
      50              55              60

Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys Arg Glu
      65              70              75              80

Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile Asp Arg
      85              90              95

Pro Val Arg Pro Leu Phe Pro Glu Gly Phe Phe Asn Glu Ile Gln Val
      100             105             110

Ile Ala Thr Val Val Ser Val Asn Pro Gln Ile Ser Pro Asp Leu Val
      115             120             125

Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val Pro Phe
      130             135             140

Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asn Asp Gln Phe
      145             150             155             160

Val Leu Asn Pro Thr Thr Ser Glu Gln Lys Ile Ser Arg Leu Asp Leu
      165             170             175

Val Val Ser Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser Glu Ala
      180             185             190

Asp Ile Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe Gly His
      195             200             205

Glu Gln Gln Gln Val Val Ile Glu Asn Ile Lys Glu Phe Val Lys Glu
      210             215             220

Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn Thr Asp
      225             230             235             240

Leu Ile Asn Lys Val Lys Ala Leu Ala Glu Thr Arg Leu Gly Asp Ala
      245             250             255

Tyr Arg Ile Val Glu Lys Gln Val Arg Tyr Glu Gln Ile Asp Ala Ile
      260             265             270

Lys Ala Glu Val Ile Ala Gln Leu Thr Ala Glu Asp Glu Thr Val Ser
      275             280             285

Glu Gly Thr Ile Ile Asp Ile Ile Thr Ala Leu Glu Ser Gln Ile Val
      290             295             300

Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr Val
      305             310             315             320

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Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Ser Val Leu Pro Arg Thr  
 325 330 335  
 His Gly Ser Ala Leu Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala Val  
 340 345 350  
 Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu Thr  
 355 360 365  
 Gly Glu Lys Ser Asp Arg Phe Leu Phe His Tyr Asn Phe Pro Pro Tyr  
 370 375 380  
 Ser Val Gly Glu Thr Gly Arg Ile Gly Ser Pro Lys Arg Arg Glu Ile  
 385 390 395 400  
 Gly His Gly Arg Leu Ala Lys Arg Gly Val Leu Ala Val Met Pro Thr  
 405 410 415  
 Ala Glu Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr Glu  
 420 425 430  
 Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu Ala  
 435 440 445  
 Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile Ala  
 450 455 460  
 Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp Ile  
 465 470 475 480  
 Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala Gly  
 485 490 495  
 Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu Gly  
 500 505 510  
 Ile Thr Pro Glu Ile Met Arg Ile Ala Leu Asn Gln Ala Lys Gly Ala  
 515 520 525  
 Arg Met His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro Arg  
 530 535 540  
 Ala Asp Ile Ser Asp Tyr Ala Pro Arg Ile His Thr Met Lys Ile Asp  
 545 550 555 560  
 Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile Arg  
 565 570 575  
 Ala Leu Thr Glu Glu Thr Asn Thr Ser Ile Asp Ile Asp Asp Gly  
 580 585 590  
 Thr Val Lys Ile Ala Ala Thr Asp Gly Asn Ala Ala Lys Ala Val Met  
 595 600 605  
 Ala Arg Ile Glu Glu Ile Val Ala Glu Val Glu Val Asn Gln Ile Tyr  
 610 615 620  
 Asn Gly Lys Val Thr Arg Val Val Asp Phe Gly Ala Phe Val Ser Ile  
 625 630 635 640  
 Leu Gly Gly Lys Glu Gly Leu Val His Ile Ser Gln Ile Thr Asn Glu  
 645 650 655

Arg Val Glu Arg Val Ala Asp Tyr Leu Thr Val Gly Gln Glu Val Gln  
 660 665 670  
 Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr Met  
 675 680 685  
 Lys Asp Ile Asn Asn Thr Asn Glu Ala Asn Ala Glu Thr Val Ala  
 690 695 700  
 Glu Asn Val Val Glu Thr Glu Gln Glu Asn Asn Phe  
 705 710 715  
  
 <210> 172  
 <211> 1517  
 <212> DNA  
 <213> Pasteurella (Mannheimia) haemolytica  
  
 <220>  
 <221> CDS  
 <222> (1)..(1515)  
  
 <220>  
 <223> purF  
  
 <400> 172  
 atg tgc ggc att gtc ggt att att ggg aat tcg ccg gtg aat cag gcg 48  
 Met Cys Gly Ile Val Gly Ile Ile Gly Asn Ser Pro Val Asn Gln Ala  
 1 5 10 15  
 att tat gat ggt tta aca tta ctt caa cac cga gga caa gat gcc gca 96  
 Ile Tyr Asp Gly Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala  
 20 25 30  
 ggt atc gtc acc ata gac gat gaa aat cgt ttc cgc tta cgc aaa gct 144  
 Gly Ile Val Thr Ile Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala  
 35 40 45  
 aac ggc tta gtc agc gat gtt ttc cag caa gag cat atg gtg aga tta 192  
 Asn Gly Leu Val Ser Asp Val Phe Gln Gln Glu His Met Val Arg Leu  
 50 55 60  
 caa ggc aat gtt gga att ggt cac gtt cgc tac cca aca gca ggt agc 240  
 Gln Gly Asn Val Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser  
 65 70 75 80  
 tca agt gtg tct gaa gcc cag cca ttt tat gtc aat tca cct ttc ggt 288  
 Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Phe Gly  
 85 90 95  
 att acc tta gtt cac aac ggt aat tta act aat aat gcg gaa ctt aaa 336  
 Ile Thr Leu Val His Asn Gly Asn Leu Thr Asn Asn Ala Glu Leu Lys  
 100 105 110  
 gct cgc tta tac aac gaa gcc cgc cgc cat gtg aac act aat tct gat 384  
 Ala Arg Leu Tyr Asn Glu Ala Arg Arg His Val Asn Thr Asn Ser Asp  
 115 120 125  
 tct gaa tcc ctt ctt aat att ttt gct tac ttt tta gat ctc tat tcc 432  
 Ser Glu Ser Leu Leu Asn Ile Phe Ala Tyr Phe Leu Asp Leu Tyr Ser  
 130 135 140  
 act cag cat tta agc cca gac aat atc ttt gaa acg gtt cgt aaa acc 480

Thr	Gln	His	Leu	Ser	Pro	Asp	Asn	Ile	Phe	Glu	Thr	Val	Arg	Lys	Thr	
145					150					155					160	
aat	gat	agc	att	cgt	ggc	gct	tat	gct	tgc	att	gcg	atg	att	atc	gga	528
Asn	Asp	Ser	Ile	Arg	Gly	Ala	Tyr	Ala	Cys	Ile	Ala	Met	Ile	Ile	Gly	
				165					170					175		
cac	ggc	atg	gtt	gct	ttc	cgt	gac	cca	ttc	ggc	att	gcg	ccg	tta	gtg	576
His	Gly	Met		180	Phe	Arg	Asp	Pro	Phe	Gly	Ile	Arg	Pro	Leu	Val	
							185						190			
ctg	ggc	aaa	cgt	gaa	atc	gag	ggc	aaa	acc	gaa	tat	atg	ttt	gct	tcg	624
Leu	Gly	Lys	Arg	Glu	Ile	Glu	Gly	Lys	Thr	Glu	Tyr	Met	Phe	Ala	Ser	
		195				200						205				
gaa	agt	gtg	gct	ctt	gat	gta	gtg	ggg	ttt	gaa	ttt	gtg	cga	gat	gtg	672
Glu	Ser	Val	Ala	Leu	Asp	Val	Val	Gly	Phe	Glu	Phe	Val	Arg	Asp	Val	
		210				215						220				
ctg	ccg	ggc	gaa	gcg	att	tat	gtt	acc	ttt	gat	ggg	caa	tta	cat	tcg	720
Leu	Pro	Gly	Glu	Ala	Ile	Tyr	Val	Thr	Phe	Asp	Gly	Gln	Leu	His	Ser	
		225			230				235					240		
caa	att	tgt	gcc	gat	aat	cca	aaa	ctg	aat	cct	tgt	att	ttt	gaa	tat	768
Gln	Ile	Cys	Ala	Asp	Asn	Pro	Lys	Leu	Asn	Pro	Cys	Ile	Phe	Glu	Tyr	
			245						250					255		
gtt	tat	ttt	gcc	cgt	cct	gat	tcc	gtc	att	gat	ggc	gtt	tct	gta	tat	816
Val	Tyr	Phe	Ala	Arg	Pro	Asp	Ser	Val	Ile	Asp	Gly	Val	Ser	Val	Tyr	
			260					265					270			
tct	gca	cga	gtg	cat	atg	ggc	gaa	tta	tta	ggc	gag	aaa	att	aaa	cgt	864
Ser	Ala	Arg	Val	His	Met	Gly	Glu	Leu	Leu	Gly	Glu	Lys	Ile	Lys	Arg	
		275				280						285				
gaa	tgg	gga	cga	att	atc	gat	gat	att	gat	gtg	gtg	atc	ccg	att	cct	912
Glu	Trp	Gly	Arg	Ile	Ile	Asp	Asp	Ile	Asp	Val	Val	Ile	Pro	Ile	Pro	
		290				295					300					
gaa	acc	tca	aat	gat	att	gcg	gta	cgt	att	gct	aat	atg	ttg	tat	aaa	960
Glu	Thr	Ser	Asn	Asp	Ile	Ala	Val	Arg	Ile	Ala	Asn	Met	Leu	Tyr	Lys	
					310					315				320		
ccc	tat	cgt	caa	ggg	ttt	gtt	aaa	aac	cgc	tat	gta	gct	cga	act	ttt	1008
Pro	Tyr	Arg	Gln	Gly	Phe	Val	Lys	Asn	Arg	Tyr	Val	Ala	Arg	Thr	Phe	
				325					330					335		
att	atg	ccg	ggg	caa	gca	cag	cgt	aaa	agc	tcg	gtt	cgc	cgt	aaa	tta	1056
Ile	Met	Pro	Gly	Gln	Ala	Gln	Arg	Lys	Ser	Ser	Val	Arg	Arg	Lys	Leu	
			340					345					350			
aat	gcg	att	gcc	tct	gaa	ttt	aaa	ggc	aaa	agc	gtg	tta	ctg	gtt	gat	1104
Asn	Ala	Ile	Ala	Ser	Glu	Phe	Lys	Gly	Lys	Ser	Val	Leu	Leu	Val	Asp	
		355					360					365				
gat	tct	att	gta	cga	ggc	aca	acg	tct	gaa	caa	atc	gtg	gaa	atg	gca	1152
Asp	Ser	Ile	Val	Arg	Gly	Thr	Thr	Ser	Glu	Gln	Ile	Val	Glu	Met	Ala	
		370				375						380				
cga	gca	gct	ggc	gca	aaa	cgg	gtt	tat	ttt	gcc	tct	gcc	gca	ccg	gaa	1200
Arg	Ala	Ala	Gly	Ala	Lys	Arg	Val	Tyr	Phe	Ala	Ser	Ala	Ala	Pro	Glu	
		385			390					395				400		

att cgc tac ccg aat gtg tat ggc att gat atg ccg act tgt gaa gaa 1248  
 Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Cys Glu Glu  
 405 410 415  
 tta gtg gct tat gat cgc tca gtg gaa gag gtt gca cag atg ata ggg 1296  
 Leu Val Ala Tyr Asp Arg Ser Val Glu Glu Val Ala Gln Met Ile Gly  
 420 425 430  
 gtg gat aaa ttg att ttc caa gac ctt gaa gca ctt tat aag tct att 1344  
 Val Asp Lys Leu Ile Phe Gln Asp Leu Glu Ala Leu Tyr Lys Ser Ile  
 435 440 445  
 caa ctg gaa aat ccg act att cat cgc ttt gat gac tct gta ttt aca 1392  
 Gln Leu Glu Asn Pro Thr Ile His Arg Phe Asp Asp Ser Val Phe Thr  
 450 455 460  
 gga gaa tat att aca ggt gat gta gat aaa tgc tat tta gac agt ata 1440  
 Gly Glu Tyr Ile Thr Gly Asp Val Asp Lys Cys Tyr Leu Asp Ser Ile  
 465 470 475 480  
 gca aga tct cga aac gat aaa gca aaa gca gag gcg gca aaa caa gcc 1488  
 Ala Arg Ser Arg Asn Asp Lys Ala Lys Ala Glu Ala Ala Lys Gln Ala  
 485 490 495  
 acc aat tta gaa att cat aac gaa aga ta 1517  
 Thr Asn Leu Glu Ile His Asn Glu Arg  
 500 505

&lt;210&gt; 173

&lt;211&gt; 505

&lt;212&gt; PRT

&lt;213&gt; Pasteurella (Mannheimia) haemolytica

&lt;400&gt; 173

Met Cys Gly Ile Val Gly Ile Ile Gly Asn Ser Pro Val Asn Gln Ala  
 1 5 10 15  
 Ile Tyr Asp Gly Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala  
 20 25 30  
 Gly Ile Val Thr Ile Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala  
 35 40 45  
 Asn Gly Leu Val Ser Asp Val Phe Gln Gln Glu His Met Val Arg Leu  
 50 55 60  
 Gln Gly Asn Val Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser  
 65 70 75 80  
 Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Phe Gly  
 85 90 95  
 Ile Thr Leu Val His Asn Gly Asn Leu Thr Asn Asn Ala Glu Leu Lys  
 100 105 110  
 Ala Arg Leu Tyr Asn Glu Ala Arg Arg His Val Asn Thr Asn Ser Asp  
 115 120 125  
 Ser Glu Ser Leu Leu Asn Ile Phe Ala Tyr Phe Leu Asp Leu Tyr Ser  
 130 135 140

Thr Gln His Leu Ser Pro Asp Asn Ile Phe Glu Thr Val Arg Lys Thr  
 145 150 155 160  
 Asn Asp Ser Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly  
 165 170 175  
 His Gly Met Val Ala Phe Arg Asp Pro Phe Gly Ile Arg Pro Leu Val  
 180 185 190  
 Leu Gly Lys Arg Glu Ile Glu Gly Lys Thr Glu Tyr Met Phe Ala Ser  
 195 200 205  
 Glu Ser Val Ala Leu Asp Val Val Gly Phe Glu Phe Val Arg Asp Val  
 210 215 220  
 Leu Pro Gly Glu Ala Ile Tyr Val Thr Phe Asp Gly Gln Leu His Ser  
 225 230 235 240  
 Gln Ile Cys Ala Asp Asn Pro Lys Leu Asn Pro Cys Ile Phe Glu Tyr  
 245 250 255  
 Val Tyr Phe Ala Arg Pro Asp Ser Val Ile Asp Gly Val Ser Val Tyr  
 260 265 270  
 Ser Ala Arg Val His Met Gly Glu Leu Leu Gly Glu Lys Ile Lys Arg  
 275 280 285  
 Glu Trp Gly Arg Ile Ile Asp Asp Ile Asp Val Val Ile Pro Ile Pro  
 290 295 300  
 Glu Thr Ser Asn Asp Ile Ala Val Arg Ile Ala Asn Met Leu Tyr Lys  
 305 310 315 320  
 Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Ala Arg Thr Phe  
 325 330 335  
 Ile Met Pro Gly Gln Ala Gln Arg Lys Ser Ser Val Arg Arg Lys Leu  
 340 345 350  
 Asn Ala Ile Ala Ser Glu Phe Lys Gly Lys Ser Val Leu Val Asp  
 355 360 365  
 Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala  
 370 375 380  
 Arg Ala Ala Gly Ala Lys Arg Val Tyr Phe Ala Ser Ala Ala Pro Glu  
 385 390 395 400  
 Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Cys Glu Glu  
 405 410 415  
 Leu Val Ala Tyr Asp Arg Ser Val Glu Glu Val Ala Gln Met Ile Gly  
 420 425 430  
 Val Asp Lys Leu Ile Phe Gln Asp Leu Glu Ala Leu Tyr Lys Ser Ile  
 435 440 445  
 Gln Leu Glu Asn Pro Thr Ile His Arg Phe Asp Asp Ser Val Phe Thr  
 450 455 460  
 Gly Glu Tyr Ile Thr Gly Asp Val Asp Lys Cys Tyr Leu Asp Ser Ile  
 465 470 475 480

Ala Arg Ser Arg Asn Asp Lys Ala Lys Ala Glu Ala Ala Lys Gln Ala  
 485 490 495

Thr Asn Leu Glu Ile His Asn Glu Arg  
 500 505

<210> 174

<211> 386

<212> DNA

<213> Pasteurella (Mannheimia) haemolytica

<220>

<221> CDS

<222> (1)..(384)

<220>

<223> yjgF

<400> 174

atg aca gtt atc cac aca gaa aat gca ccg gca gcg att ggg cct tat 48  
 Met Thr Val Ile His Thr Glu Asn Ala Pro Ala Ala Ile Gly Pro Tyr  
 1 5 10 15

gtg caa gca gtt gat tta ggc aat atg gtt tta act tct ggg caa att 96  
 Val Gln Ala Val Asp Leu Gly Asn Met Val Leu Thr Ser Gly Gln Ile  
 20 25 30

ccc gtg aat cct gaa acc ggc gaa atc ccg agt gat att gtg caa caa 144  
 Pro Val Asn Pro Glu Thr Gly Glu Ile Pro Ser Asp Ile Val Gln Gln  
 35 40 45

acc cgc caa tct ctg aac aac gtg aaa gcc att atc gaa caa gcc ggc 192  
 Thr Arg Gln Ser Leu Asn Asn Val Lys Ala Ile Ile Glu Gln Ala Gly  
 50 55 60

tta acc gtt gcc gat att gta aag acc acc gta ttt gtc aaa gat ctt 240  
 Leu Thr Val Ala Asp Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu  
 65 70 75 80

aac gac ttc gca aag gta aat gcg gaa tac caa gcc ttc ttc caa gaa 288  
 Asn Asp Phe Ala Lys Val Asn Ala Glu Tyr Gln Ala Phe Phe Gln Glu  
 85 90 95

aac gaa cac cct aat ttt ccg gct cgt tct tgc gta gaa gtg gct cgt 336  
 Asn Glu His Pro Asn Phe Pro Ala Arg Ser Cys Val Glu Val Ala Arg  
 100 105 110

tta cca aaa gat gtt ggc att gag atc gaa gcg att gca gta cgc cga 384  
 Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala Val Arg Arg  
 115 120 125

ta 386

<210> 175

<211> 128

<212> PRT

<213> Pasteurella (Mannheimia) haemolytica

<400> 175

Met Thr Val Ile His Thr Glu Asn Ala Pro Ala Ala Ile Gly Pro Tyr  
 1 5 10 15

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Val Gln Ala Val Asp Leu Gly Asn Met Val Leu Thr Ser Gly Gln Ile
      20                      25                      30
Pro Val Asn Pro Glu Thr Gly Glu Ile Pro Ser Asp Ile Val Gln Gln
      35                      40                      45
Thr Arg Gln Ser Leu Asn Asn Val Lys Ala Ile Ile Glu Gln Ala Gly
      50                      55                      60
Leu Thr Val Ala Asp Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu
      65                      70                      75                      80
Asn Asp Phe Ala Lys Val Asn Ala Glu Tyr Gln Ala Phe Phe Gln Glu
      85                      90                      95
Asn Glu His Pro Asn Phe Pro Ala Arg Ser Cys Val Glu Val Ala Arg
      100                     105                     110
Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala Val Arg Arg
      115                     120                     125

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&lt;210&gt; 176

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt;

&lt;222&gt;

&lt;223&gt; Description of Artificial Sequence: PRIMER

&lt;400&gt; 176

atggcnggng cnaargarat

20

&lt;210&gt; 177

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt;

&lt;222&gt;

&lt;223&gt; Description of Artificial Sequence: PRIMER

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 3

&lt;223&gt; n = A or T or G or C

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 12

&lt;223&gt; n = A or T or G or C

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 15

&lt;223&gt; n = A or T or G or C

&lt;400&gt; 177

gcngcyttca tngcnaccat

20

&lt;210&gt; 178

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<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
<221> misc_feature
<222> 3
<223> N = A or T or G or C

<400> 178
ggnTTYatyc ayaaaaayat g                21

<210> 179
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
<221> misc_feature
<222> 6
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 12
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 15
<223> N = A or T or G or C

<400> 179
tcttngtra tngtnacatc rtg                23

<210> 180
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 180
gcsggyaac crcgttgga ttgg                24

<210> 181
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 181
ccctaarat rtctgaaagc accac                25

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<210> 182
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
<221> misc_feature
<222> 9
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 15
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 18
<223> N = A or T or G or C

<400> 182
atgtgyggna tygtnggnat                                20

<210> 183
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 183
catatcaata ccatacacat t                                21

<210> 184
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
<221> misc_feature
<222> 3
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 6
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 12
<223> N = A or T or G or C

<400> 184
ggnccntayg tncarg                                      16

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<210> 185
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
<221> misc_feature
<222> 1
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 4
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 10
<223> N = A or T or G or C

<400> 185
ngcnacytcn acrca 15

<210> 186
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 186
gaagccgcc aacgctcttg gg 22

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 187
gttgcttctt ttgcttcac tgg 23

<210> 188
<211> 24
<212> DNA
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<220>
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LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,  
MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG,  
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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: ANTI-BACTERIAL VACCINE COMPOSITIONS

(57) Abstract: Gram negative bacterial virulence genes are identified, thereby allowing the identification of anti-bacterial agents that target these virulence genes and their products, and the provision of gram negative bacterial mutants useful in vaccines.

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## INTERNATIONAL SEARCH REPORT

International Application No  
PCT/US 02/01971

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N1/20 A61K39/102 A61K35/74 C12N15/31 C12N15/63  
C07K14/285 C07K16/12 C12Q1/18 G01N33/68

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N A61K C07K C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EMBL, EPO-Internal, WPI Data, BIOSIS, MEDLINE

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL [Online] 10 February 2001 (2001-02-10) MAY B.J. ET AL.: "Pasteurella multocida PM70 section 152 of 204 of the complete genome" Database accession no. AE006064 XP002224305 nucleotides 3352-4146	1-41
X	& DATABASE EMBL [Online] Entry AE006064, 10 February 2001 (2001-02-10) MAY B.J. ET AL.: "Pasteurella multocida PM70 section 31 of 204 of the complete genome" the whole document	5-23,25, 28
A	& BARBARA J. MAY ET AL.: "Complete genomic sequence of Pasteurella multocida, Pm70" PROCEEDINGS OF THE NATIONAL ACADEMY OF -/--	1-41

☒ Further documents are listed in the continuation of box C.☐ Patent family members are listed in annex.

## \* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the international search

12 May 2003

Date of mailing of the international search report

16. 05. 2003

Name and mailing address of the ISA

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Authorized officer

Montero Lopez, B

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>SCIENCES OF USA, vol. 98, no. 6, 13 March 2001 (2001-03-13), pages 3460-3465, XP002202785 WASHINGTON US page 3463, right-hand column, paragraph 2 -page 3464, left-hand column, paragraph 1 ---</p> <p>COONEY ET AL: "Three contiguous lipoprotein genes in Pasteurella haemolytica A1 which are homologous to a lipoprotein gene in Haemophilus influenza Type b" INFECTION AND IMMUNITY, AMERICAN SOCIETY OF MICROBIOLOGY, WASHINGTON, DC, US, vol. 61, no. 11, November 1993 (1993-11), pages 4682-4688, XP002148894 ISSN: 0019-9567 abstract page 4683, left-hand column, last paragraph -page 4685, left-hand column, paragraph 1; figures 3,4 page 4686, right-hand column, paragraph 2 ---</p>	<p>5-23,25, 28</p>
A	<p>TROY E. FULLER ET AL.: "Identification of Pasteurella multocida virulence genes in a septicemic mouse model using signature-tagged mutagenesis" MICROBIAL PATHOGENESIS, vol. 29, 2000, pages 25-38, XP002224304 the whole document -----</p>	<p>1-41</p>

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US 02/01971**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:  
1-41 partially
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-41 partially

Gram-negative bacteria comprising a mutation in a gene of sequence SEQ ID NO:1 resulting in decreased activity of the gene product; immunogenic composition comprising the bacteria; method of producing such mutant bacteria; nucleotide sequence comprising SEQ ID NO:1, vector and host cell comprising the same and use thereof to produce a polypeptide; encoded polypeptide of sequence SEQ ID NO:2; antibody against it; use of the polypeptide of sequence SEQ ID NO:2 for identifying antibacterial agents.

2. Claims: 1-41 partially

Idem as subject 1 for, respectively sequences SEQ ID NO:3 and 4; 7 and 8; 9 and 10; 21 and 22; 25 and 26.

3. Claims: 1-4, 21-23, 27, 28 partially

Gram-negative bacteria comprising a mutation in a gene of sequence SEQ ID NO:27 resulting in decreased activity of the gene product; immunogenic composition comprising the bacteria; nucleotide sequence comprising SEQ ID NO:27.

4. Claims: 1-41 partially

Idem as subject 1 for, respectively, sequences SEQ ID NOs:29 and 30; 39 and 40; 41 and 42; 51 and 52; 53 and 54; 55 and 56.

5. Claims: 1-28 partially

Gram-negative bacteria comprising a mutation in a gene of sequence SEQ ID NO:57 resulting in decreased activity of the gene product; immunogenic composition comprising the bacteria; method of producing such mutant bacteria; nucleotide sequence comprising SEQ ID NO:57.

6. Claims: 1-41 partially

Idem as subject 1 for, respectively sequences SEQ ID NOs:58 and 59; 60 and 61; 68 and 69; 72 and 73; 74 and 75; 76 and 77; 78 and 79; 80 and 81; 82 and 83; 84 and 85; 104 and 105; 108 and 109; 112 and 113; 116 and 117; 118 and 119; 120 and 121; 122 and 123; 124 and 125; 126 and 127; 128 and 129; 130 and 131

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

## 7. Claims: 5-26, 29-41 partially

Attenuated Pasteurellaceae bacteria comprising a mutation in a gene of sequence SEQ ID NO:11; immunogenic composition containing it; method of producing such mutant bacteria; nucleotide sequence comprising SEQ ID NO:11, vector and host cell comprising the same and use thereof to produce a polypeptide; encoded polypeptide of sequence SEQ ID NO:12; antibody against it; use of the polypeptide of sequence SEQ ID NO:12 for identifying antibacterial agents.

## 8. Claims: 5-26, 28-41 partially

Idem as subject 36 for, respectively, sequences SEQ ID NOs:13 and 14; 15 and 16; 17 and 18; 19 and 20; 23 and 24; 31 and 32; 33 and 34; 35 and 36; 37 and 38; 70 and 71; 100 and 101; 102 and 103; 106 and 107; 110 and 111; 114 and 115; 132 and 133; 134 and 135; 136 and 137; 138 and 139; 140 and 141; 142 and 143; 144 and 145; 146 and 147; 148 and 149; 150 and 151; 152 and 153; 154 and 155; 156 and 157; 158 and 159; 160 and 161

## 9. Claims: 5-26 partially

Attenuated Pasteurellaceae bacteria comprising a mutation in, respectively a gene of sequence SEQ ID NO:162 and 163; immunogenic composition containing it; method of producing such mutant bacteria; nucleotide sequence comprising SEQ ID NO:162 or 163.

## 10. Claims: 5-26, 28-41 partially

Idem as subject 36 for, respectively, sequences SEQ ID NOs:164 and 165; 166 and 167; 168 and 169; 170 and 171; 172 and 173; 174 and 175

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09/809,665 15 March 2001 (15.03.2001) US(71) Applicant (for all designated States except US): PHAR-  
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[US/US]; 2364 Quincy Avenue, Portage, MI 49024 (US).(74) Agent: WILLIAMS, Joseph, A., Jr.; Marshall, Gerstein  
& Borun, 6300 Sears Tower, 233 South Wacker Drive,  
Chicago, IL 60606 (US).(81) Designated States (national): AE, AG, AL, AM, AT, AU,  
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CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,  
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,  
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,  
MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG,  
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European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR,  
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(BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,  
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ance Notes on Codes and Abbreviations" appearing at the begin-  
ning of each regular issue of the PCT Gazette.

(54) Title: ANTI-BACTERIAL VACCINE COMPOSITIONS

(57) Abstract: Gram negative bacterial virulence genes are identified, thereby allowing the identification of anti-bacterial agents that target these virulence genes and their products, and the provision of gram negative bacterial mutants useful in vaccines.

WO 02/075507 A3

## AMENDED CLAIMS

[received by the International Bureau on 11 July 2003 (11.07.03)  
original claims 1 to 41 have been amended by claims 1 to 29]

## WHAT IS CLAIMED IS:

1. An attenuated *Mannheimia* bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOS: 166, 168, 170, 172 and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.
2. The *Mannheimia* bacteria of claim 1 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.
3. The *Mannheimia* bacteria of claim 1 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.
4. The *Mannheimia* bacteria of claim 1 wherein said mutation results in deletion of all or part of said gene.
5. The *Mannheimia* bacteria of claim 1 wherein the *Mannheimia bacteria* is *Mannheimia haemolytica*.
6. The *Mannheimia* bacteria of claim 5 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.
7. The *Mannheimia* bacteria of claim 5 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.
8. The *Mannheimia* bacteria of claim 5 wherein said mutation results in deletion of all or part of said gene.
9. An immunogenic composition comprising the bacteria according to any one of claims 1 through 8.

10. A vaccine composition comprising the immunogenic composition according to claim 9 and a pharmaceutically acceptable carrier.

11. The vaccine composition according to claim 10 further comprising an  
5 adjuvant.

12. A method for producing a gram-negative bacteria mutant comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOS: 166, 168, 170, 172, and 174 or a species homolog  
10 thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

13. A method for producing an attenuated *Mannheimia* bacteria comprising the step of introducing a mutation in a gene represented by a nucleotide  
15 sequence set forth in any one of SEQ ID NOS: 166, 168, 170, 172, and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

14. A purified and isolated *Mannheimia* polynucleotide comprising a  
20 nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOS: 166, 168, 170, 172 and 174.

15. A purified and isolated *Mannheimia* polynucleotide comprising a  
nucleotide sequence as set forth in SEQ ID NO: 166.  
25

16. A purified and isolated polynucleotide encoding a *Mannheimia* virulence gene product, or species homolog thereof, selected from the group consisting of:

- a) the polynucleotide according to claim 14;

b) polynucleotides encoding a polypeptide encoded by the polynucleotide of (a); and

c) polynucleotides that hybridize to the complement of the polynucleotides of (a) or (b) under moderate stringency conditions.

5

17. A purified and isolated *Mannheimia* polynucleotide encoding a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOS: 167, 169, 171, 173, and 175.

10

18. The polynucleotide of claim 17 which is a DNA.

19. A vector comprising the DNA of claim 18.

20. The vector of claim 19 that is an expression vector, wherein the DNA  
15 is operatively linked to an expression control DNA sequence.

21. A host cell stably transformed or transfected with the DNA of claim 18 in a manner allowing the expression of the encoded polypeptide in said host cell.

20

22. A method for producing a recombinant polypeptide comprising culturing the host cell of claim 21 in a nutrient medium and isolating the encoded polypeptide from said host cell or said nutrient medium.

23. A purified polypeptide produced by the method of claim 22.

25

24. A purified polypeptide comprising a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOS: 167, 169, 171, 173, and 175.

24. 25. An antibody that is specifically reactive with the polypeptide of claim

26. The antibody of claim 25 that is a monoclonal antibody.

5

27. A method of using the monoclonal antibody of claim 26 for identifying a bacteria of claims 1 or 5, comprising the steps of contacting an extract of bacteria with said monoclonal antibody and detecting the absence of binding of said monoclonal antibody.

10

28. A method of identifying an anti-bacterial agent comprising the steps of assaying potential agents for the ability to interfere with expression or activity of gene products represented by the amino acid sequences set forth in any one of SEQ ID NOS: 167, 169, 171, 173, and 175 and identifying an agent that interferes with expression or activity of said gene products.

15

29. A method of identifying an anti-bacterial agent comprising the steps of:

- 20 a) measuring expression or activity of a gene product as set out in any one of SEQ ID NOS: 167, 169, 171, 173, and 175;
- b) contacting the gene product in (a) with a test compound;
- c) measuring expression or activity of the gene product in the presence of the test compound; and
- 25 d) identifying the test compound as an antibacterial agent when expression or activity of the gene product is decreased in the presence of the test compound as compared to expression or activity in the absence of the test compound.